FORM PTO-1390 (Modified) (REV 5-93) U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371

ATTORNEY'S DOCKET NUMBER: 032931-0253

U.S. APPLICATION NO. (If known, see 37 C.F.R. 1.5): Unassigned 09/868987

INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/CA99/01230	December 23, 1999	December 23, 1998

TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES THEREOF

APPLICANT(S) FOR DO/EO/US: Andrew D. MURDIN, Raymond P. OOMEN and Joe WANG

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.
3. ☐ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
   - ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
   - ☒ has been transmitted by the International Bureau.
   - ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
   - ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
   - ☐ have been transmitted by the International Bureau.
   - ☐ have not been made; however, the time limit for making such amendments has NOT expired.
   - ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☐ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).
11. ☐ Applicant claims small entity status under 37 CFR 1.27 .

Items 12. to 17. below concern other document(s) or information included:

12. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
13. ☒ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
14. ☒ A FIRST preliminary amendment.
    ☐ A SECOND or SUBSEQUENT preliminary amendment.
15. ☐ A substitute specification.
16. ☐ A change of power of attorney and/or address letter.
17. ☐ Other items or information:

U.S. APPLICATION NO. (If known, see 37 CFR 1.5)	INTERNATIONAL APPLICATION NO.	ATTORNEY'S DOCKET NUMBER
Unassigned 09/868987	PCT/CA99/01230	032931-0253

18. ☒ The following fees are submitted:	CALCULATIONS	PTO USE ONLY
Basic National Fee (37 CFR 1.492(a)(1)-(5): Search Report has been prepared by the EPO or JPO.....$860.00		
International preliminary examination fee paid to USPTO (37 CFR 1.482).....$690.00		
No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2) $710.00		
Neither international preliminary examination fee (37 CFR 1.482) nor International search fee (37 CFR 1.445(a)(2)) paid to USPTO $1,000.00		
International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4) $100.00		
ENTER APPROPRIATE BASIC FEE AMOUNT =	$860.00	
Surcharge of $130.00 for furnishing the oath or declaration later than 20 Months from the earliest claimed priority date (37 CFR 1.492(e))		

Claims	Number Filed		Included in Basic Fee		Extra Claims		Rate		
Total Claims	39	-	20	=	19	×	$18.00	$342.00	
Independent Claims	9	-	3	=	6	×	$80.00	$480.00	
Multiple dependent claim(s) (if applicable)							$270.00		
TOTAL OF ABOVE CALCULATIONS =								$1682.00	
Reduction by ½ for filing by small entity, if applicable.								$0.00	
SUBTOTAL =								$1682.00	
Processing fee of $130.00 for furnishing English translation later the 20 months from the earliest claimed priority date (37 CFR 1.492(f). +									
TOTAL NATIONAL FEE =								$1682.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). $40.00 per property +								$40.00	
TOTAL FEES ENCLOSED =								$1722.00	

				Amount to be:	
				Refunded	$
				Charged	$

a. ☒ A check in the amount of $1722.00 to cover the above fees is enclosed.

b. ☐ Please charge my Deposit Account No. 19-0741 in the amount of $.00 to the above fees. A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 19-0741. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

Foley & Lardner
Washington Harbour
3000 K Street, N.W., Suite 500
Washington, D.C. 20007-5109

SIGNATURE

NAME MICHELE M. SIMKIN

REGISTRATION NUMBER 34,717

Docket No. 032931-0253

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Andrew D. MURDIN, et al.
Title:	CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES THEREOF
Application No.:	To be assigned (US entry of PCT/CA99/01230)
Filing Date:	December 23, 1999
Examiner:	Unassigned
Art Unit:	Unassigned

PRELIMINARY AMENDMENT

Commissioner for Patents
Washington, D.C. 20231

Sir:

In accordance with 37 CFR §1.121, please cancel claims 40-78 in their entirety without prejudice or disclaimer and substitute for claims 1-39 in the Annex to the IPER the following rewritten versions of the same claims, as amended. The changes to claims 1-39 are shown explicitly in the attached "marked up claims".

IN THE CLAIMS:

1. (Amended) A nucleic acid molecule comprising a nucleic acid sequence which encodes a polypeptide selected from any one of:

(a) SEQ ID Nos: 15 to 26;

(b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and

(c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

2. (Amended) A nucleic acid molecule comprising a nucleic acid sequence selected from any of:

(a) SEQ ID Nos: 2 to 13;

(b) a sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 2 to 13;

(c) a sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (a) and (b); and

(d) a sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to any one of the polypeptides encoded by SEQ ID Nos: 2 to 13.

3. (Amended) A nucleic acid molecule comprising a nucleic acid sequence which is anti-sense to the nucleic acid molecule of claim 1.

4. (Amended) A nucleic acid molecule comprising a nucleic acid sequence which encodes a fusion protein, said fusion protein comprising a polypeptide encoded by a nucleic acid molecule according to claim 1 and a second polypeptide.

5. (Amended) The nucleic acid molecule of claim 4 wherein the second polypeptide is a heterologous signal peptide.

6. (Amended) The nucleic acid molecule of claim 4 wherein the second polypeptide has adjuvant activity.

7. (Amended) A nucleic acid molecule according to claim 1, operatively linked to one or more expression control sequences.

8. (Amended) A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any of:

(i) SEQ ID Nos: 1 to 13;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iii) a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (i) and (ii);

(iv) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(v) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(vi) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vii) a nucleic acid sequence which encodes a polypeptide as defined in (i) to (v) or an immunogenic fragment as defined in (vi) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (v) or the corresponding fragment of (vi);

wherein each first nucleic acid is capable of being expressed.

9. (Amended) A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined in (i) to (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence

to the corresponding polypeptide of (i) to (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

10. (Amended) The vaccine of claim 9 wherein the second polypeptide is a heterologous signal peptide.

11. (Amended) The vaccine of claim 9 wherein the second polypeptide has adjuvant activity.

12. (Amended) The vaccine of any one of claim 8 wherein each first nucleic acid is operatively linked to one or more expression control sequences.

13. (Amended) A vaccine according to claim 8 wherein each first nucleic acid is expressed as a polypeptide, and wherein the vaccine comprises a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

14. (Amended) The vaccine according to claim 13 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

15. (Amended) A pharmaceutical composition comprising a nucleic acid according to claim 1 and a pharmaceutically acceptable carrier.

16. (Amended) A pharmaceutical composition comprising a vaccine according to claim 8 and a pharmaceutically acceptable carrier.

17. (Amended) A unicellular host transformed with the nucleic acid molecule of claim 7.

18. (Amended) An isolated nucleic acid probe of 5 to 100 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

19. (Amended) An isolated primer of 10 to 40 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

20. (Amended) A polypeptide encoded by a nucleic acid sequence according to claim 2.

21. (Amended) A polypeptide comprising an amino acid sequence selected from any one of:

(a) SEQ ID Nos: 15 to 26;

(b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and

(c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

22. (Amended) A fusion protein comprising a polypeptide of claim 21 and a second polypeptide.

23. (Amended) The fusion protein of claim 22 wherein the second polypeptide is a heterologous signal peptide.

24. (Amended) The fusion protein of claim 22 wherein the second polypeptide has adjuvant activity.

25. (Amended) A method for producing a polypeptide of claim 21, comprising the step of culturing a unicellular host transformed with a nucleic acid encoding a polypeptide of claim 21.

26. (Amended) An antibody against the polypeptide of claim 21.

27. (Amended) A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined in (i) to (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (iv) or the corresponding fragment of (v).

28. (Amended) A vaccine comprising at least one fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined in (i) to (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (iv) or the corresponding fragment of (v); and

(b) a second polypeptide.

29. (Amended) The vaccine of claim 28 wherein the second polypeptide is a heterologous signal peptide.

30. (Amended) The vaccine of claim 28 wherein the second polypeptide has adjuvant activity.

31. (Amended) A vaccine comprising at least one first polypeptide according to claim 20 and an additional polypeptide which enhances the immune response to the first polypeptide.

32. (Amended) The vaccine of claim 31 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

33. (Amended) A pharmaceutical composition comprising a polypeptide according to claim 20 and a pharmaceutically acceptable carrier.

34. (Amended) A pharmaceutical composition comprising a vaccine according to claim 27 and a pharmaceutically acceptable carrier.

35. (Amended) A pharmaceutical composition comprising an antibody according to claim 26 and a pharmaceutically acceptable carrier.

36. (Amended) A method for preventing or treating *Chlamydia* infection comprising administering to a patient an effective amount of:

(a) a nucleic acid according to claim 2;

(b) a vaccine comprising a vaccine vector and at least one first nucleic acid according to claim 2;

(c) a pharmaceutical composition comprising a nucleic acid according to claim 2 and a pharmaceutically acceptable carrier;

(d) a polypeptide encoded by a nucleic acid according to claim 2; or

(e) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.

37. (Amended) A method of detecting *Chlamydia* infection comprising the step of assaying a body fluid of a mammal to be tested, with a component selected from any one of:

(a) a nucleic acid according to claim 2;

(b) a polypeptide encoded by a nucleic acid according to claim 2; and

(c) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.

38. (Amended) A diagnostic kit comprising instructions for use and a component selected from any one of:

(a) a nucleic acid according to claim 2;

(b) a polypeptide encoded by a nucleic acid according to claim 2; and

(c) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.

39. (Amended) A method for identifying a polypeptide of claim 20 which induces an immune response effective to prevent or lessen the severity of *Chlamydia* infection in a mammal previously immunized with polypeptide, comprising the steps of:

(a) immunizing a mouse with the polypeptide of claim 20; and

(b) inoculating the immunized mouse with *Chlamydia;*

wherein the polypeptide or fusion protein which prevents or lessens the severity of *Chlamydia* infection in the immunized mouse compared to a non-immunized control mouse is identified.

REMARKS

Applicant respectfully requests that the foregoing amendments to the claims be entered in order to avoid this application incurring a surcharge for the presence of one or more multiple dependent claims and to improve clarity.

Respectfully submitted,

Date: June 22, 2001

By S. G. Kent, Reg #24768

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MARKED UP CLAIMS

1. A nucleic acid molecule comprising a nucleic acid sequence which encodes a polypeptide selected from any one of:

(a) SEQ ID Nos: 15 to 26;

(b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and

(c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

2. A nucleic acid molecule comprising a nucleic acid sequence selected from any of:

(a) SEQ ID Nos: 2 to 13;

(b) a sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 2 to 13;

(c) a sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (a) and (b); and

(d) a sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to any one of the polypeptides encoded by SEQ ID Nos: 2 to 13.

3. A nucleic acid molecule comprising a nucleic acid sequence which is anti-sense to the nucleic acid molecule of claim 1~~ or 2~~.

4. A nucleic acid molecule comprising a nucleic acid sequence which encodes a fusion protein, said fusion protein comprising a polypeptide encoded by a nucleic acid molecule according to claim 1 and a second polypeptide.

5. The nucleic acid molecule of claim 4 wherein the second polypeptide is a heterologous signal peptide.

6. The nucleic acid molecule of claim 4 wherein the second polypeptide has adjuvant activity.

7. A nucleic acid molecule according to ~~any one of claims 1 to 6,~~claim 1, operatively linked to one or more expression control sequences.

8. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any of:

(i) SEQ ID Nos: 1 to 13;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iii) a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (i) and (ii);

(iv) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(v) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(vi) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vii) a nucleic acid sequence which encodes a polypeptide as defined in (i) to (v) or an immunogenic fragment as defined in (vi) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (v) or the corresponding fragment of (vi);

wherein each first nucleic acid is capable of being ~~expressed and wherein the vaccine optionally comprises a second nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune~~ expressed. ~~response to the polypeptide expressed by the first nucleic acid.~~

9. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined in (i) to (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being ~~expressed and wherein the vaccine optionally comprises a second nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune~~ expressed.

~~response to the first polypeptide.~~

10. The vaccine of claim 9 wherein the second polypeptide is a heterologous signal peptide.

11. The vaccine of claim 9 wherein the second polypeptide has adjuvant activity.

12. The vaccine of any one of ~~claims 8 to 11 wherein~~claim 8 wherein each first nucleic acid is operatively linked to one or more expression control sequences.

13. A vaccine~~comprising at least one first nucleic acid~~ according to ~~any one of claims 1, 2, and 4 to 7 and a vaccine vector~~claim 8 wherein each first nucleic acid is expressed as a polypeptide, and wherein the vaccine~~optionally comprising~~comprises a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by ~~said~~the first nucleic acid.

14. The vaccine ~~of any one of claims 8 to~~according to claim 13 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

15. A pharmaceutical composition comprising a nucleic acid according to ~~any one of claims 1 to 7~~claim 1 and a pharmaceutically acceptable carrier.

16. A pharmaceutical composition comprising a vaccine according to ~~any one of claims 8 to 14~~claim 8 and a pharmaceutically acceptable carrier.

17. A unicellular host transformed with the nucleic acid molecule of claim 7.

18. An isolated nucleic acid probe of 5 to 100 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

19. An isolated primer of 10 to 40 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

20. A polypeptide encoded by a nucleic acid sequence according to ~~any one of claims 1, 2 and 4 to 7.~~claim 2.

21. A polypeptide comprising an amino acid sequence selected from any one of:

(a) SEQ ID Nos: 15 to 26;

(b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and

(c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

22. A fusion protein comprising a polypeptide of claim~~20 or~~ 21 and a second polypeptide.

23. The fusion protein of claim 22 wherein the second polypeptide is a heterologous signal peptide.

24. The fusion protein of claim 22 wherein the second polypeptide has adjuvant activity.

25. A method for producing a polypeptide of claim ~~20 or~~ 21, ~~or a fusion protein of any one of claims 22 to 24,~~ comprising the step of culturing a unicellular host transformed with a nucleic acid encoding a polypeptide of claim ~~17.~~21.

26. An antibody against the polypeptide of claim ~~20 or 21, or against a fusion protein of any one of claims 22 to 24.~~21.

27. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined in (i) to (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (iv) or the corresponding fragment of ~~(v);~~(v).

~~wherein the vaccine optionally comprises an additional polypeptide which enhances the immune response to the first polypeptide.~~

28. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

~~(iii) a~~(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined in (i) to (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) to (iv) or the corresponding fragment of (v); and

(b) a second~~polypeptide;~~

~~wherein the vaccine optionally comprises an additional polypeptide which enhances the immune response to the first~~ polypeptide.

29. The vaccine of claim 28 wherein the second polypeptide is a heterologous signal peptide.

30. The vaccine of claim 28 wherein the second polypeptide has adjuvant activity.

31. A vaccine comprising at least one first polypeptide according to ~~any one of claims 20 to 24, optionally~~

~~comprising~~claim 20 and an additional polypeptide which enhances the immune response to the first polypeptide.

32. The vaccine of ~~any one of claims 27 to~~claim 31 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

33. A pharmaceutical composition comprising a polypeptide according to ~~any one of claims~~claim 20~~to 24~~ and a pharmaceutically acceptable carrier.

34. A pharmaceutical composition comprising a vaccine according to ~~any one of claims~~claim 27~~to 32~~ and a pharmaceutically acceptable carrier.

35. A pharmaceutical composition comprising an antibody according to claim 26 and a pharmaceutically acceptable carrier.

36. A method for preventing or treating *Chlamydia* infection ~~using:~~comprising administering to a patient an effective amount of:

~~(a) the nucleic acid of any one of claims 1 to 7;~~

~~(b) the vaccine of any one of claims 8 to 14 and 27 to 32;~~ (a) a nucleic acid according to claim 2;

(b) a vaccine comprising a vaccine vector and at least one first nucleic acid according to claim 2;

~~(c) the~~ (c) a pharmaceutical composition ~~of any one of claims 15, 16 and 33 to 35;~~comprising a nucleic acid according to claim 2 and a pharmaceutically acceptable carrier;

~~(d) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; or~~

~~(c) the antibody of claim 26.~~ (d) a polypeptide encoded by a nucleic acid according to claim 2; or

(e) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.

37. A method of detecting *Chlamydia* infection comprising the step of assaying a body fluid of a mammal to be tested, with a component selected from any one of:

~~(a) the nucleic acid of any one of claims 1 to 7;~~
~~(b) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; and~~
~~(c) the antibody of claim 26.~~

(a) a nucleic acid according to claim 2;

(b) a polypeptide encoded by a nucleic acid according to claim 2; and

(c) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.

38. A diagnostic kit comprising instructions for use and a component selected from any one of:

~~(a) the nucleic acid of any one of claims 1 to 7;~~
~~(b) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; and~~
~~(c) the antibody of claim 26.~~

(a) a nucleic acid according to claim 2;

(b) a polypeptide encoded by a nucleic acid according to claim 2; and

(c) an antibody against a polypeptide encoded by a nucleic acid according to claim 2.

39. A method for identifying a polypeptide of claim 20~~or 21, or a fusion protein of any one of claims 22 to 24~~ which

induces an immune response effective to prevent or lessen the severity of *Chlamydia* infection in a mammal previously immunized with polypeptide, comprising the steps of:

(a) immunizing a mouse with the polypeptide ~~or fusion protein;~~of claim 20; and

(b) inoculating the immunized mouse with *Chlamydia;* wherein the polypeptide or fusion protein which prevents or lessens the severity of *Chlamydia* infection in the immunized mouse compared to a non-immunized control mouse is identified.

TITLE OF INVENTION

CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES THEREOF

REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of 13 U.S. provisional applications: U.S. Provisional Application Nos. 60/113,280, 60/113,281, 60/113,282, 60/113,283, 60/113,284, 60/113,285, 60/113,385, all of which were filed December 23, 1998; and U.S. Provisional Application Nos.60/114,050, 60/114,056, 60/114,057, 60/114,058, 60/114,059, 60/114,061, all of which were filed December 28, 1998.

FIELD OF INVENTION

The present invention relates to *Chlamydia* antigens and corresponding DNA molecules, which can be used to prevent and treat *Chlamydia* infection in mammals, such as humans.

BACKGROUND OF THE INVENTION

Chlamydiae are prokaryotes. They exhibit morphologic and structural similarities to gram-negative bacteria including a trilaminar outer membrane, which contains lipopolysaccharide and several membrane proteins that are structurally and functionally analogous to proteins found in *E coli*. They are obligate intra-cellular parasites with a unique biphasic life cycle consisting of a metabolically inactive but infectious extracellular stage and a replicating but non-infectious intracellular stage. The replicative stage of the life-cycle takes place within a membrane-bound inclusion which sequesters the bacteria away from the cytoplasm of the infected host cell.

C. pneumoniae is a common human pathogen, originally described as the TWAR strain of *Chlamydia psittaci* but subsequently recognised to be a new species. *C. pneumoniae* is antigenically, genetically and morphologically distinct from

other chlamydia species (*C. trachomatis, C. pecorum* and *C. psittaci*). It shows 10% or less DNA sequence homology with either of *C. trachomatis* or *C. psittaci*.

C. pneumoniae is a common cause of community acquired pneumonia, only less frequent than *Streptococcus pneumoniae* and *Mycoplasma pneumoniae* (Grayston *et al.* (1995) Journal of Infectious Diseases 168:1231; Campos *et al.* (1995) Investigation of Ophthalmology and Visual Science 36:1477). It can also cause upper respiratory tract symptoms and disease, including bronchitis and sinusitis (Grayston *et al.* (1995) Journal of Infectious Diseases 168:1231; Grayston *et al* (1990) Journal of Infectious Diseases 161:618; Marrie (1993) Clinical Infectious Diseases. 18:501; Wang *et al* (1986) Chlamydial infections. Cambridge University Press, Cambridge. p. 329. The great majority of the adult population (over 60%) has antibodies to *C. pneumoniae* (Wang *et al* (1986) Chlamydial infections. Cambridge University Press, Cambridge. p. 329), indicating past infection which was unrecognized or asymptomatic.

C. pneumoniae infection usually presents as an acute respiratory disease (*i.e.*, cough, sore throat, hoarseness, and fever; abnormal chest sounds on auscultation). For most patients, the cough persists for 2 to 6 weeks, and recovery is slow. In approximately 10% of these cases, upper respiratory tract infection is followed by bronchitis or pneumonia. Furthermore, during a *C. pneumoniae* epidemic, subsequent co-infection with pneumococcus has been noted in about half of these pneumonia patients, particularly in the infirm and the elderly. As noted above, there is more and more evidence that *C. pneumoniae* infection is also linked to diseases other than respiratory infections.

The reservoir for the organism is presumably people. In contrast to *C. psittaci* infections, there is no known bird or animal reservoir. Transmission has not been clearly defined.

It may result from direct contact with secretions, from fomites, or from airborne spread. There is a long incubation period, which may last for many months. Based on analysis of epidemics, *C. pneumoniae* appears to spread slowly through a population (case-to-case interval averaging 30 days) because infected persons are inefficient transmitters of the organism. Susceptibility to *C. pneumoniae* is universal. Reinfections occur during adulthood, following the primary infection as a child. *C. pneumoniae* appears to be an endemic disease throughout the world, noteworthy for superimposed intervals of increased incidence (epidemics) that persist for 2 to 3 years. *C. trachomatis* infection does not confer cross-immunity to *C. pneumoniae*. Infections are easily treated with oral antibiotics, tetracycline or erythromycin (2 g/d, for at least 10 to 14 d). A recently developed drug, azithromycin, is highly effective as a single-dose therapy against chlamydial infections.

In most instances, *C. pneumoniae* infection is often mild and without complications, and up to 90% of infections are subacute or unrecognized. Among children in industrialized countries, infections have been thought to be rare up to the age of 5 y, although a recent study (E Normann *et al*, Chlamydia pneumoniae in children with acute respiratory tract infections, Acta Paediatrica, 1998, Vol 87, Iss 1, pp 23-27) has reported that many children in this age group show PCR evidence of infection despite being seronegative, and estimates a prevalence of 17-19% in 2-4 y olds. In developing countries, the seroprevalence of *C. pneumoniae* antibodies among young children is elevated, and there are suspicions that *C. pneumoniae* may be an important cause of acute lower respiratory tract disease and mortality for infants and children in tropical regions of the world.

From seroprevalence studies and studies of local epidemics, the initial *C. pneumoniae* infection usually happens

between the ages of 5 and 20 y. In the USA, for example, there are estimated to be 30,000 cases of childhood pneumonia each year caused by *C. pneumoniae*. Infections may cluster among groups of children or young adults (*e.g.*, school pupils or military conscripts).

C. pneumoniae causes 10 to 25% of community-acquired lower respiratory tract infections (as reported from Sweden, Italy, Finland, and the USA). During an epidemic, *C. pneumonia* infection may account for 50 to 60% of the cases of pneumonia. During these periods, also, more episodes of mixed infections with *S. pneumoniae* have been reported.

Reinfection during adulthood is common; the clinical presentation tends to be milder. Based on population seroprevalence studies, there tends to be increased exposure with age, which is particularly evident among men. Some investigators have speculated that a persistent, asymptomatic *C. pneumoniae* infection state is common.

In adults of middle age or older, *C. pneumoniae* infection may progress to chronic bronchitis and sinusitis. A study in the USA revealed that the incidence of pneumonia caused by *C. pneumoniae* in persons younger than 60 years is 1 case per 1,000 persons per year; but in the elderly, the disease incidence rose three-fold. *C. pneumoniae* infection rarely leads to hospitalization, except in patients with an underlying illness.

Of considerable importance is the association of atherosclerosis and *C. pneumoniae* infection. There are several epidemiological studies showing a correlation of previous infections with *C. pneumoniae* and heart attacks, coronary artery and carotid artery disease (Saikku *et al.*(1988) Lancet; ii:983; Thom *et al.* (1992) JAMA 268:68; Linnanmaki *et al.* (1993), Circulation 87:1030; Saikku *et al.* (1992) Annals Internal Medicine 116:273; Melnick *et al* (1993) American Journal of Medicine 95:499). Moreover, the organisms have been detected in

atheromas and fatty streaks of the coronary, carotid, peripheral arteries and aorta (Shor *et al.* (1992) South African. Medical Journal 82:158; Kuo *et al.* (1993) Journal of Infectious Diseases 167:841; Kuo *et al.* (1993) Arteriosclerosis and Thrombosis 13:1500; Campbell *et al* (1995) Journal of Infectious Diseases 172:585; Chiu *et al.* Circulation, 1997 (In Press)). Viable *C. pneumoniae* has been recovered from the coronary and carotid artery (Ramirez *et al* (1996) Annals of Internal Medicine 125:979; Jackson *et al.* Abst. K121, p272, 36th ICAAC, 15-18 Sept. 1996, New Orleans). Furthermore, it has been shown that *C. pneumoniae* can induce changes of atherosclerosis in a rabbit model (Fong *et al* (1997) Journal of Clinical Microbiolology 35:48). Taken together, these results indicate that it is highly probable that *C. pneumoniae* can cause atherosclerosis in humans, though the epidemiological importance of chlamydial atherosclerosis remains to be demonstrated.

A number of recent studies have also indicated an association between *C. pneumoniae* infection and asthma. Infection has been linked to wheezing, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults, and small-scale studies have shown that prolonged antibiotic treatment was effective at greatly reducing the severity of the disease in some individuals (Hahn DL, *et al.* Evidence for Chlamydia pneumoniae infection in steroid-dependent asthma. Ann Allergy Asthma Immunol. 1998 Jan; 80(1): 45-49; Hahn DL, *et al.* Association of Chlamydia pneumoniae IgA antibodies with recently symptomatic asthma. Epidemiol Infect. 1996 Dec; 117(3): 513-517; Bjornsson E, *et al.* Serology of chlamydia in relation to asthma and bronchial hyperresponsiveness. Scand J Infect Dis. 1996; 28(1): 63-69; Hahn DL. Treatment of *Chlamydia pneumoniae* infection in adult asthma: a before-after trial. J Fam Pract. 1995 Oct; 41(4): 345-351; Allegra L, *et al.* Acute exacerbations of asthma in adults: role of Chlamydia pneumoniae infection. Eur Respir J. 1994 Dec; 7(12): 2165-2168; Hahn DL,

et al. Association of Chlamydia pneumoniae (strain TWAR) infection with wheezing, asthmatic bronchitis, and adult-onset asthma. JAMA. 1991 Jul 10; 266(2): 225-230).

In light of these results a protective vaccine against *C. pneumoniae* infection would be of considerable importance. There is not yet an effective vaccine for any human chlamydial infection. It is conceivable that an effective vaccine can be developed using physically or chemically inactivated Chlamydiae. However, such a vaccine does not have a high margin of safety. In general, safer vaccines are made by genetically manipulating the organism by attenuation or by recombinant means. Accordingly, a major obstacle in creating an effective and safe vaccine against human chlamydial infection has been the paucity of genetic information regarding Chlamydia, specifically *C. pneumoniae*.

Studies with *C. trachomatis* and *C. psittaci* indicate that safe and effective vaccine against Chlamydia is an attainable goal. For example, mice which have recovered from a lung infection with *C. trachomatis* are protected from infertility induced by a subsequent vaginal challenge (Pal *et al*.(1996) Infection and Immunity.64:5341). Similarly, sheep immunized with inactivated *C. psittaci* were protected from subsequent chlamydial-induced abortions and stillbirths (Jones *et al*. (1995) Vaccine 13:715). Protection from chlamydial infections has been associated with Th1 immune responses, particularly the induction of INFg - producing CD4+T-cells (Igietsemes *et al*. (1993) Immunology 5:317). The adoptive transfer of CD4+ cell lines or clones to nude or SCID mice conferred protection from challenge or cleared chronic disease (Igietseme *et al* (1993) Regional Immunology 5:317; Magee *et al* (1993) Regional Immunology 5: 305), and *in vivo* depletion of CD4+ T cells exacerbated disease post-challenge (Landers *et al* (1991) Infection & Immunity 59:3774; Magee *et al* (1995) Infection & Immunity 63:516). However, the presence of

sufficiently high titres of neutralising antibody at mucosal surfaces can also exert a protective effect (Cotter *et al.* (1995) Infection and Immunity 63:4704).

Antigenic variation within the species *C. pneumoniae* is not well documented due to insufficient genetic information, though variation is expected to exist based on *C. trachomatis*. Serovars of *C. trachomatis* are defined on the basis of antigenic variation in the major outer membrane protein (MOMP), but published *C. pneumoniae* MOMP gene sequences show no variation between several diverse isolates of the organism (Campbell *et al* (1990) Infection and Immunity 58:93; McCafferty *et al* (1995) Infection and Immunity 63:2387-9; Gaydos *et al* (1992) Infection and Immunity 60(12):5319-5323). Regions of the protein known to be conserved in other chlamydial MOMPs are conserved in *C. pneumoniae* (Campbell *et al* (1990) Infection and Immunity 58:93; McCafferty *et al* (1995) Infection and Immunity 63:2387-9). One study has described a strain of *C. pneumoniae* with a MOMP of greater that usual molecular weight, but the gene for this has not been sequenced (Grayston *et al.* (1995) Journal of Infectious Diseases 168:1231). Partial sequences of outer membrane protein 2 from nine diverse isolates were also found to be invariant (Ramirez *et al* (1996) Annals of Internal Medicine 125:979). The genes for HSP60 and HSP70 show little variation from other chlamydial species, as would be expected. The gene encoding a 76kDa antigen has been cloned from a single strain of *C. pneumoniae*. It has no significant similarity with other known chlamydial genes (Marrie (1993) Clinical Infectious Diseases. 18:501).

Many antigens recognised by immune sera to *C. pneumoniae* are conserved across all chlamydiae, but 98kDa, 76 kDa and 54 kDa proteins appear to be *C. pneumoniae*-specific (Campos *et al.* (1995) Investigation of Ophthalmology and Visual Science 36:1477; Marrie (1993) Clinical Infectious Diseases. 18:501; Wiedmann-Al-Ahmad M, *et al.* Reactions of polyclonal and

neutralizing anti-p54 monoclonal antibodies with an isolated, species-specific 54-kilodalton protein of Chlamydia pneumoniae. Clin Diagn Lab Immunol. 1997 Nov; 4(6): 700-704).

Immunoblotting of isolates with sera from patients does show variation of blotting patterns between isolates, indicating that serotypes *C. pneumoniae* may exist (Grayston et al. (1995) Journal of Infectious Diseases 168:1231; Ramirez *et al* (1996) Annals of Internal Medicine 125:979). However, the results are potentially confounded by the infection status of the patients, since immunoblot profiles of a patient's sera change with time post-infection. An assessment of the number and relative frequency of any serotypes, and the defining antigens, is not yet possible.

Accordingly, a need exists for identifying and isolating polynucleotide sequences of *C. pneumoniae* for use in preventing and treating Chlamydia infection.

SUMMARY OF THE INVENTION

The present invention provides purified and isolated polynucleotide molecules that encode *Chlamydia* polypeptides which can be used in methods to prevent, treat, and diagnose *Chlamydia* infection. In one form of the invention, the polynucleotide molecules are selected from DNA that encode polypeptides CPN100686 RY 54(SEQ ID No: 1), CPN100696 RY-55(SEQ ID No: 2), CPN100709 RY-57 (SEQ ID No: 3), CPN100710 RY-58 (SEQ ID No:4), CPN100711 RY-59 (SEQ ID No: 5), CPN100877 RY-61 (SEQ ID No:6), CPN100325 RY-62 (SEQ ID No:7), CPN100368 RY-63 (SEQ ID No:8), CPN100624 RY-64 (SEQ ID No:9), CPN100633 RY-65 (SEQ ID No:10), CPN100985 RY-66 (SEQ ID No:11),, CPN100987 RY-67 (SEQ ID No:12) and CPN100988 RY-68 (SEQ ID No:13). Another form of the invention provides polypeptides corresponding to the isolated DNA molecules. The amino acid sequences of the corresponding encoded polypeptides are shown for CPN100686 RY 54 as SEQ ID No: 14, CPN100696 RY-55 as SEQ ID No: 15, CPN100709 RY-57 as SEQ ID

No: 16, CPN100710 RY-58 as SEQ ID No: 17, CPN100711 RY-59 as SEQ ID No: 18, CPN100877 RY-61 as SEQ ID No: 19, CPN100325 RY-62 as SEQ ID No: 20, CPN100368 RY-63 as SEQ ID No: 21, CPN100624 RY-64 as SEQ ID No: 22, CPN100633 RY-65 as SEQ ID No: 23, CPN100985 RY-66 as SEQ ID No: 24, CPN100987 RY-67 as SEQ ID No: 24 and CPN100988 RY-68 as SEQ ID No: 26.

Those skilled in the art will readily understand that the invention, having provided the polynucleotide sequences encoding *Chlamydia* polypeptides, also provides polynucleotides encoding fragments derived from such peptides. Moreover, the invention is understood to provide mutants and derivatives of such polypeptides and fragments derived therefrom, which result from the addition, deletion, or substitution of non-essential amino acids as described herein. Those skilled in the art would also readily understand that the invention, having provided the polynucleotide sequences encoding Chlamydia polypeptides, further provides monospecific antibodies that specifically bind to such polypeptides.

The present invention has wide application and includes expression cassettes, vectors, and cells transformed or transfected with the polynucleotides of the invention. Accordingly, the present invention further provides (i) a method for producing a polypeptide of the invention in a recombinant host system and related expression cassettes, vectors, and transformed or transfected cells; (ii) a vaccine, or a live vaccine vector such as a pox virus, *Salmonella typhimurium*, or *Vibrio cholerae* vector, containing a polynucleotide of the invention, such vaccines and vaccine vectors being useful for, *e.g.*, preventing and treating *Chlamydia* infection, in combination with a diluent or carrier, and related pharmaceutical compositions and associated therapeutic and/or prophylactic methods; (iii) a therapeutic and/or prophylactic use of an RNA or DNA molecule of the invention, either in a naked form or formulated with a delivery vehicle, a polypeptide

or combination of polypeptides, or a monospecific antibody of the invention, and related pharmaceutical compositions; (iv) a method for diagnosing the presence of *Chlamydia* in a biological sample, which can involve the use of a DNA or RNA molecule, a monospecific antibody, or a polypeptide of the invention; and (v) a method for purifying a polypeptide of the invention by antibody-based affinity chromatography.

BRIEF DESCRIPTION OF THE DRAWINGS

The present invention will be further understood from the following description with reference to the drawings, in which:

Figure 1 through 13 show the restriction enzyme analysis of the nucleic acid sequences of the invention.

Figures 14 through 26 show an identification of T and B cell epitopes from the amino acid sequences SEQ ID Nos: 14 to 26.

DETAILED DESCRIPTION OF INVENTION

Open reading frames (ORFs) encoding chlamydial polypeptides have been identified from the *C. pneumoniae* genome. These polypeptides include polypeptides found permanently in the bacterial membrane structure, polypeptides present in the external vicinity of the bacterial membrane, polypeptides found permanently in the inclusion membrane structure, polypeptides present in the external vicinity of the inclusion membrane, and polypeptides released into the cytoplasm of the infected cell. These polypeptides can be used to prevent and treat *Chlamydia* infection.

The polypeptide CPN100686 RY 54 whose amino acid sequence is shown as SEQ ID No: 14 is a putative 98 kDa outer membrane protein; the polypeptide CPN100696 RY-55 (SEQ ID No: 15) is consistent with a sulfur-rich protein; the polypeptide CPN100709 RY-57 (SEQ ID No: 16) is a ABC transporter; the polypeptide CPN100710 RY-58 (SEQ ID No: 17) is an adhesion

protein; the polypeptide CPN100711 RY-59 (SEQ ID No: 18) is a putative outer membrane protein; the polypeptide CPN100877 RY-61 (SEQ ID No: 19) is a putative 98 kDa outer membrane protein, and so are the polypeptides CPN100325 RY-62 (SEQ ID No: 20), CPN100368 RY-63 (SEQ ID No: 21), CPN100624 RY-64 (SEQ ID No: 22),and CPN100633 RY-65 (SEQ ID No: 23); the polypeptide CPN100985 RY-66 (SEQ ID No: 24) is yscT; and CPN100988 RY-68 (SEQ ID No: 26) is a flagellar protein.

According to a first aspect of the invention, isolated polynucleotides are provided which encode the precursor and mature forms of *Chlamydia* polypeptides, whose amino acid sequences are selected from the group consisting of SEQ ID Nos: 14 to 26.

The term "isolated polynucleotide" is defined as a polynucleotide removed from the environment in which it naturally occurs. For example, a naturally-occurring DNA molecule present in the genome of a living bacteria or as part of a gene bank is not isolated, but the same molecule separated from the remaining part of the bacterial genome, as a result of, *e.g.*, a cloning event (amplification), is isolated. Typically, an isolated DNA molecule is free from DNA regions (*e.g.*, coding regions) with which it is immediately contiguous at the 5' or 3' end, in the naturally occurring genome. Such isolated polynucleotides may be part of a vector or a composition and still be defined as isolated in that such a vector or composition is not part of the natural environment of such polynucleotide.

The polynucleotides of the invention are either RNA or DNA (cDNA, genomic DNA, or synthetic DNA), or modifications, variants, homologs or fragments thereof. The DNA is either double-stranded or single-stranded, and, if single-stranded, is either the coding strand or the non-coding (anti-sense) strand. Any one of the sequences that encode the polypeptides of the invention as shown in SEQ ID Nos: 1 to 13 is (a) a coding

sequence, (b) a ribonucleotide sequence derived from transcription of (a), or (c) a coding sequence which uses the redundancy or degeneracy of the genetic code to encode the same polypeptides. By "polypeptide" or "protein" is meant any chain of amino acids, regardless of length or post-translational modification (*e.g.*, glycosylation or phosphorylation). Both terms are used interchangeably in the present application.

Consistent with the first aspect of the invention, amino acid sequences are provided which are homologous to any one of SEQ ID Nos: 14 to 26. As used herein, "homologous amino acid sequence" is any polypeptide which is encoded, in whole or in part, by a nucleic acid sequence which hybridizes at 25-35°C below critical melting temperature (Tm), to any portion of the nucleic acid sequences of SEQ ID Nos: 1 to 13. A homologous amino acid sequence is one that differs from an amino acid sequence shown in any one of SEQ ID Nos: 13 to 26 by one or more conservative amino acid substitutions. Such a sequence also encompass serotypic variants (defined below) as well as sequences containing deletions or insertions which retain inherent characteristics of the polypeptide such as immunogenicity. Preferably, such a sequence is at least 75%, more preferably 80%, and most preferably 90% identical to any one of SEQ ID Nos: 14 to 26.

Homologous amino acid sequences include sequences that are identical or substantially identical to SEQ ID Nos: 14 to 26. By "amino acid sequence substantially identical" is meant a sequence that is at least 90%, preferably 95%, more preferably 97%, and most preferably 99% identical to an amino acid sequence of reference and that preferably differs from the sequence of reference by a majority of conservative amino acid substitutions.

Conservative amino acid substitutions are substitutions among amino acids of the same class. These classes include, for example, amino acids having uncharged polar side chains, such as

asparagine, glutamine, serine, threonine, and tyrosine; amino acids having basic side chains, such as lysine, arginine, and histidine; amino acids having acidic side chains, such as aspartic acid and glutamic acid; and amino acids having nonpolar side chains, such as glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan, and cysteine.

Homology is measured using sequence analysis software such as Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705. Amino acid sequences are aligned to maximize identity. Gaps may be artificially introduced into the sequence to attain proper alignment. Once the optimal alignment has been set up, the degree of homology is established by recording all of the positions in which the amino acids of both sequences are identical, relative to the total number of positions.

Homologous polynucleotide sequences are defined in a similar way. Preferably, a homologous sequence is one that is at least 45%, more preferably 60%, and most preferably 85% identical to any one of coding sequences SEQ ID Nos: 1 to 13.

Consistent with the first aspect of the invention, polypeptides having a sequence homologous to any one of SEQ ID Nos: 14 to 26 include naturally-occurring allelic variants, as well as mutants or any other non-naturally occurring variants that retain the inherent characteristics of the polypeptide of SEQ ID Nos: 14 to 26.

As is known in the art, an allelic variant is an alternate form of a polypeptide that is characterized as having a substitution, deletion, or addition of one or more amino acids that does not alter the biological function of the polypeptide. By "biological function" is meant the function of the polypeptide in the cells in which it naturally occurs, even if the function is not necessary for the growth or survival of the

cells. For example, the biological function of a porin is to allow the entry into cells of compounds present in the extracellular medium. Biological function is distinct from antigenic property. A polypeptide can have more than one biological function.

Allelic variants are very common in nature. For example, a bacterial species such as *C. pneumoniae*, is usually represented by a variety of strains that differ from each other by minor allelic variations. Indeed, a polypeptide that fulfills the same biological function in different strains can have an amino acid sequence (and polynucleotide sequence) that is not identical in each of the strains. Despite this variation, an immune response directed generally against many allelic variants has been demonstrated. In studies of the *Chlamydial* MOMP antigen, cross-strain antibody binding plus neutralization of infectivity occurs despite amino acid sequence variation of MOMP from strain to strain, indicating that the MOMP, when used as an immunogen, is tolerant of amino acid variations.

Polynucleotides encoding homologous polypeptides or allelic variants are retrieved by polymerase chain reaction (PCR) amplification of genomic bacterial DNA extracted by conventional methods. This involves the use of synthetic oligonucleotide primers matching upstream and downstream of the 5' and 3' ends of the encoding domain. Suitable primers are designed according to the nucleotide sequence information provided in SEQ ID Nos: 1 to 13. The procedure is as follows: a primer is selected which consists of 10 to 40, preferably 15 to 25 nucleotides. It is advantageous to select primers containing C and G nucleotides in a proportion sufficient to ensure efficient hybridization; *i.e.*, an amount of C and G nucleotides of at least 40%, preferably 50% of the total nucleotide content. A standard PCR reaction contains typically 0.5 to 5 Units of Taq DNA polymerase per 100 µL, 20 to 200 µM deoxynucleotide each,

preferably at equivalent concentrations, 0.5 to 2.5 MM magnesium over the total deoxynucleotide concentration, 10^5 to 10^6 target molecules, and about 20 pmol of each primer. About 25 to 50 PCR cycles are performed, with an annealing temperature 15°C to 5°C below the true Tm of the primers. A more stringent annealing temperature improves discrimination against incorrectly annealed primers and reduces incorportion of incorrect nucleotides at the 3' end of primers. A denaturation temperature of 95°C to 97°C is typical, although higher temperatures may be appropriate for dematuration of G+C-rich targets. The number of cycles performed depends on the starting concentration of target molecules, though typically more than 40 cycles is not recommended as non-specific background products tend to accumulate.

An alternative method for retrieving polynucleotides encoding homologous polypeptides or allelic variants is by hybridization screening of a DNA or RNA library. Hybridization procedures are well-known in the art and are described in Ausubel *et al.*, (Ausubel *et al.*, Current Protocols in Molecular Biology, John Wiley & Sons Inc., 1994), Silhavy *et al.* (Silhavy *et al.* Experiments with Gene Fusions, Cold Spring Harbor Laboratory Press, 1984), and Davis *et al.* (Davis *et al.* A Manual for Genetic Engineering: Advanced Bacterial Genetics, Cold Spring Harbor Laboratory Press, 1980)). Important parameters for optimizing hybridization conditions are reflected in a formula used to obtain the critical melting temperature above which two complementary DNA strands separate from each other (Casey & Davidson, Nucl. Acid Res. (1977) 4:1539). For polynucleotides of about 600 nucleotides or larger, this formula is as follows: Tm = 81.5 + 0.5 x (% G+C) + 1.6 log (positive ion concentration) - 0.6 x (% formamide). Under appropriate stringency conditions, hybridization temperature (Th) is approximately 20 to 40°C, 20 to 25°C, or, preferably 30 to 40°C

below the calculated Tm. Those skilled in the art will understand that optimal temperature and salt conditions can be readily determined.

For the polynucleotides of the invention, stringent conditions are achieved for both pre-hybridizing and hybridizing incubations (i) within 4-16 hours at 42°C, in 6 x SSC containing 50% formamide, or (ii) within 4-16 hours at 65°C in an aqueous 6 x SSC solution (1 M NaCl, 0.1 M sodium citrate (pH 7.0)).

Useful homologs and fragments thereof that do not occur naturally are designed using known methods for identifying regions of an antigen that are likely to tolerate amino acid sequence changes and/or deletions. As an example, homologous polypeptides from different species are compared; conserved sequences are identified. The more divergent sequences are the most likely to tolerate sequence changes. Homology among sequences may be analyzed using the BLAST homology searching algorithm of Altschul et al., Nucleic Acids Res.25:3389-3402 (1997). Alternatively, sequences are modified such that they become more reactive to T- and/or B-cells. (See Figures 11 to 15 below for identification of T- and B- epitopes). Yet another alternative is to mutate a particular amino acid residue or sequence within the polypeptide *in vitro*, then screen the mutant polypeptides for their ability to prevent or treat Chlamydia infection according to the method outlined below.

A person skilled in the art will readily understand that by following the screening process of this invention, it will be determined without undue experimentation whether a particular homolog of any of SEQ ID Nos: 14 to 26 may be useful in the prevention or treatment of Chlamydia infection. The screening procedure comprises the steps:

(i) immunizing an animal, preferably mouse, with the test homolog or fragment;

(ii) inoculating the immunized animal with Chlamydia; and,

(iii) selecting those homologs or fragments which confer protection against Chlamydia.

By "conferring protection" is meant that there is a reduction in severity of any of the effects of Chlamydia infection, in comparison with a control animal which was not immunized with the test homolog or fragment.

It has been previously demonstrated (Yang, Z. P., Chi, E. Y., Kuo, C. C. and Grayston, J. T. 1993. A mouse model of *C. pneumoniae* strain TWAR pneumonitis. 61(5):2037-2040) that mice are susceptible to intranasal infection with different isolates of *C. pneumoniae*. Strain AR-39 (Chi, E. Y., Kuo, C. C. and Grayston, J. T., 1987. Unique ultrastructure in the elementary body of Chlamydia sp. strain TWAR. J. Bacteriol. 169(8):3757-63) was used in Balb/c mice as a challenge infection model to examine the capacity of chlamydia gene products delivered as naked DNA to elicit a protective response against a sublethal *C. pneumoniae* lung infection. Protective immunity is defined as an accelerated clearance of pulmonary infection.

Groups of 7 to 9 week old male Balb/c mice (6 to 10 per group) were immunized intramuscularly (i.m.) plus intranasally (i.n.) with plasmid DNA containing the coding sequence of a *C. pneumoniae* polypeptide. Saline or the plasmid vector lacking an inserted chlamydial gene was given to groups of control animals.

For i.m. immunization, alternate left and right quadriceps were injected with 100µg of DNA in 50µl of PBS on three occasions at 0, 3 and 6 weeks. For i.n. immunization, anaesthetized mice aspirated 50µl of PBS containing 50 µg DNA on three occasions at 0, 3 and 6 weeks. At week 8, immunized mice were inoculated i.n. with 5×10^5 IFU of *C. pneumoniae*, strain AR39 in 100µl of SPG buffer to test their ability to limit the growth of a sublethal *C. pneumoniae* challenge.

Lungs were taken from mice at day 9 post-challenge and immediately homogenised in SPG buffer (7.5% sucrose, 5mM glutamate, 12.5mM phosphate pH7.5). The homogenate was stored frozen at -70°C until assay. Dilutions of the homogenate were assayed for the presence of infectious chlamydia by inoculation onto monolayers of susceptible cells. The inoculum was centrifuged onto the cells at 3000rpm for 1 hour, then the cells were incubated for three days at 35°C in the presence of 1µg/ml cycloheximide. After incubation the monolayers were fixed with formalin and methanol then immunoperoxidase stained for the presence of chlamydial inclusions using convalescent sera from rabbits infected with *C. pneumoniae* and metal-enhanced DAB as a peroxidase substrate.

Consistent with the first aspect of the invention, polypeptide derivatives are provided that are partial sequences of SEQ ID Nos: 14 to 26, partial sequences of polypeptide sequences homologous to SEQ ID Nos: 14 to 26, polypeptides derived from full-length polypeptides by internal deletion, and fusion proteins.

It is an accepted practice in the field of immunology to use fragments and variants of protein immunogens as vaccines, as all that is required to induce an immune response to a protein is a small (*e.g.*, 8 to 10 amino acid) immunogenic region of the protein. Various short synthetic peptides corresponding to surface-exposed antigens of pathogens other than *Chlamydia* have been shown to be effective vaccine antigens against their respective pathogens, *e.g.* an 11 residue peptide of murine mammary tumor virus (Casey & Davidson, Nucl. Acid Res. (1977) 4:1539), a 16-residue peptide of Semliki Forest virus (Snijders *et al.*, 1991. J. Gen. Virol. 72:557-565), and two overlapping peptides of 15 residues each from canine parvovirus (Langeveld *et al.*, Vaccine 12(15):1473-1480, 1994).

Accordingly, it will be readily apparent to one skilled in the art, having read the present description, that partial

sequences of SEQ ID Nos: 14 to 26 or their homologous amino acid sequences are inherent to the full-length sequences and are taught by the present invention. Such polypeptide fragments preferably are at least 12 amino acids in length. Advantageously, they are at least 20 amino acids, preferably at least 50 amino acids, more preferably at least 75 amino acids, and most preferably at least 100 amino acids in length.

Polynucleotides of 30 to 600 nucleotides encoding partial sequences of sequences homologous to SEQ ID Nos: 14 to 26 are retrieved by PCR amplification using the parameters outlined above and using primers matching the sequences upstream and downstream of the 5' and 3' ends of the fragment to be amplified. The template polynucleotide for such amplification is either the full length polynucleotide homologous to one of SEQ ID Nos: 1 to 13, or a polynucleotide contained in a mixture of polynucleotides such as a DNA or RNA library. As an alternative method for retrieving the partial sequences, screening hybridization is carried out under conditions described above and using the formula for calculating Tm. Where fragments of 30 to 600 nucleotides are to be retrieved, the calculated Tm is corrected by subtracting (600/polynucleotide size in base pairs) and the stringency conditions are defined by a hybridization temperature that is 5 to 10°C below Tm. Where oligonucleotides shorter than 20-30 bases are to be obtained, the formula for calculating the Tm is as follows: Tm = 4 x (G+C) + 2 (A+T). For example, an 18 nucleotide fragment of 50% G+C would have an approximate Tm of 54°C. Short peptides that are fragments of SEQ. ID Nos. 14 to 26 or their homologous sequences, are obtained directly by chemical synthesis (E. Gross and H. J. Meinhofer, 4 The Peptides: Analysis, Synthesis, Biology; Modern Techniques of Peptide Synthesis, John Wiley & Sons (1981), and M. Bodanzki, Principles of Peptide Synthesis, Springer -Verlag (1984)).

Useful polypeptide derivatives, *e.g.*, polypeptide fragments, are designed using computer-assisted analysis of amino acid sequences. This identifies probable surface-exposed, antigenic regions (Hughes *et al.*, 1992. Infect. Immun. 60(9):3497). An analysis of the 6 amino acid sequences contained in SEQ ID Nos: 14 to 26, based on the product of flexibility and hydrophobicity propensities using the program SEQSEE (Wishart DS, et al. "SEQSEE: a comprehensive program suite for protein sequence analysis." *Comput Appl Biosci.* 1994 Apr;10(2):121-32), reveal a number of potential B- and T-cell epitopes which may be used as a basis for selecting useful immunogenic fragments and variants. The results are shown in Figures 11 to 15. This analysis uses a reasonable combination of external surface features that is likely to be recognized by antibodies. Probable T-cell epitopes for HLA-A0201 MHC subclass were revealed by an algorithm written at Connaught Laboratories that emulates an approach developed at the NIH (Parker KC, *et al.* "Peptide binding to MHC class I molecules: implications for antigenic peptide prediction." *Immunol Res* 1995;14(1):34-57).

Epitopes which induce a protective T cell-dependent immune response are present throughout the length of the polypeptide. However, some epitopes may be masked by secondary and tertiary structures of the polypeptide. To reveal such masked epitopes large internal deletions are created which remove much of the original protein structure and expose the masked epitopes. Such internal deletions sometimes effect the additional advantage of removing immunodominant regions of high variability among strains.

Polynucleotides encoding polypeptide fragments and polypeptides having large internal deletions are constructed using standard methods (Ausubel *et al.*, Current Protocols in Molecular Biology, John Wiley & Sons Inc., 1994). Such methods include standard PCR, inverse PCR, restriction enzyme treatment of cloned DNA molecules, or the method of Kunkel *et al.*

(Kunkel *et al.* Proc. Natl. Acad. Sci. USA (1985) 82:448). Components for these methods and instructions for their use are readily available from various commercial sources such as Stratagene. Once the deletion mutants have been constructed, they are tested for their ability to prevent or treat Chlamydia infection as described above.

As used herein, a fusion polypeptide is one that contains a polypeptide or a polypeptide derivative of the invention fused at the N- or C-terminal end to any other polypeptide (hereinafter referred to as a peptide tail). A simple way to obtain such a fusion polypeptide is by translation of an in-frame fusion of the polynucleotide sequences, *i.e.*, a hybrid gene. The hybrid gene encoding the fusion polypeptide is inserted into an expression vector which is used to transform or transfect a host cell. Alternatively, the polynucleotide sequence encoding the polypeptide or polypeptide derivative is inserted into an expression vector in which the polynucleotide encoding the peptide tail is already present. Such vectors and instructions for their use are commercially available, *e.g.* the pMal-c2 or pMal-p2 system from New England Biolabs, in which the peptide tail is a maltose binding protein, the glutathione-S-transferase system of Pharmacia, or the His-Tag system available from Novagen. These and other expression systems provide convenient means for further purification of polypeptides and derivatives of the invention.

An advantageous example of a fusion polypeptide is one where the polypeptide or homolog or fragment of the invention is fused to a polypeptide having adjuvant activity, such as subunit B of either cholera toxin or *E. coli* heat-labile toxin. Another advantageous fusion is one where the polypeptide, homolog or fragment is fused to a strong T-cell epitope or B-cell epitope. Such an epitope may be one known in the art (*e.g.* the Hepatitis B virus core antigen, D.R. Millich et al., "Antibody production to the nucleocapsid and envelope of the Hepatitis B virus primed

by a single synthetic T cell site", Nature. 1987. 329:547-549), or one which has been identified in another polypeptide of the invention (Figures 11-15). Consistent with this aspect of the invention is a fusion polypeptide comprising T- or B-cell epitopes from one of SEQ ID Nos: 14 to 26 or its homolog or fragment, wherein the epitopes are derived from multiple variants of said polypeptide or homolog or fragment, each variant differing from another in the location and sequence of its epitope within the polypeptide. Such a fusion is effective in the prevention and treatment of Chlamydia infection since it optimizes the T- and B-cell response to the overall polypeptide, homolog or fragment.

To effect fusion, the polypeptide of the invention is fused to the N-, or preferably, to the C-terminal end of the polypeptide having adjuvant activity or T- or B-cell epitope. Alternatively, a polypeptide fragment of the invention is inserted internally within the amino acid sequence of the polypeptide having adjuvant activity. The T- or B-cell epitope may also be inserted internally within the amino acid sequence of the polypeptide of the invention.

Consistent with the first aspect, the polynucleotides of the invention also encode hybrid precursor polypeptides containing heterologous signal peptides, which mature into polypeptides of the invention. By "heterologous signal peptide" is meant a signal peptide that is not found in naturally-occurring precursors of polypeptides of the invention.

A polynucleotide molecule according to the invention, including RNA, DNA, or modifications or combinations thereof, has various applications. A DNA molecule is used, for example, (i) in a process for producing the encoded polypeptide in a recombinant host system, (ii) in the construction of vaccine vectors such as poxviruses, which are further used in methods and compositions for preventing and/or treating *Chlamydia* infection, (iii) as a vaccine agent (as well as an RNA

molecule), in a naked form or formulated with a delivery vehicle and, (iv) in the construction of attenuated *Chlamydia* strains that can over-express a polynucleotide of the invention or express it in a non-toxic, mutated form.

Accordingly, a second aspect of the invention encompasses (i) an expression cassette containing a DNA molecule of the invention placed under the control of the elements required for expression, in particular under the control of an appropriate promoter; (ii) an expression vector containing an expression cassette of the invention; (iii) a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, as well as (iv) a process for producing a polypeptide or polypeptide derivative encoded by a polynucleotide of the invention, which involves culturing a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, under conditions that allow expression of the DNA molecule of the invention and, recovering the encoded polypeptide or polypeptide derivative from the cell culture.

A recombinant expression system is selected from procaryotic and eucaryotic hosts. Eucaryotic hosts include yeast cells (*e.g.*, *Saccharomyces cerevisiae* or *Pichia pastoris*), mammalian cells (*e.g.*, COS1, NIH3T3, or JEG3 cells), arthropods cells (*e.g.*, *Spodoptera frugiperda* (SF9) cells), and plant cells. A preferred expression system is a procaryotic host such as *E. coli*. Bacterial and eucaryotic cells are available from a number of different sources including commercial sources to those skilled in the art, *e.g.*, the American Type Culture Collection (ATCC; Rockville, Maryland). Commercial sources of cells used for recombinant protein expression also provide instructions for usage of the cells.

The choice of the expression system depends on the features desired for the expressed polypeptide. For example, it

may be useful to produce a polypeptide of the invention in a particular lipidated form or any other form.

One skilled in the art would readily understand that not all vectors and expression control sequences and hosts would be expected to express equally well the polynucleotides of this invention. With the guidelines described below, however, a selection of vectors, expression control sequences and hosts may be made without undue experimentation and without departing from the scope of this invention.

In selecting a vector, the host must be chosen that is compatible with the vector which is to exist and possibly replicate in it. Considerations are made with respect to the vector copy number, the ability to control the copy number, expression of other proteins such as antibiotic resistance. In selecting an expression control sequence, a number of variables are considered. Among the important variable are the relative strength of the sequence (*e.g.* the ability to drive expression under various conditions), the ability to control the sequence's function, compatibility between the polynucleotide to be expressed and the control sequence (*e.g.* secondary structures are considered to avoid hairpin structures which prevent efficient transcription). In selecting the host, unicellular hosts are selected which are compatible with the selected vector, tolerant of any possible toxic effects of the expressed product, able to secrete the expressed product efficiently if such is desired, to be able to express the product in the desired conformation, to be easily scaled up, and to which ease of purification of the final product.

The choice of the expression cassette depends on the host system selected as well as the features desired for the expressed polypeptide. Typically, an expression cassette includes a promoter that is functional in the selected host system and can be constitutive or inducible; a ribosome binding site; a start codon (ATG) if necessary; a region encoding a

signal peptide, *e.g.*, a lipidation signal peptide; a DNA molecule of the invention; a stop codon; and optionally a 3' terminal region (translation and/or transcription terminator). The signal peptide encoding region is adjacent to the polynucleotide of the invention and placed in proper reading frame. The signal peptide-encoding region is homologous or heterologous to the DNA molecule encoding the mature polypeptide and is compatible with the secretion apparatus of the host used for expression. The open reading frame constituted by the DNA molecule of the invention, solely or together with the signal peptide, is placed under the control of the promoter so that transcription and translation occur in the host system. Promoters and signal peptide encoding regions are widely known and available to those skilled in the art and include, for example, the promoter of *Salmonella typhimurium* (and derivatives) that is inducible by arabinose (promoter araB) and is functional in Gram-negative bacteria such as *E. coli* (as described in U.S. Patent No. 5,028,530 and in Cagnon *et al.*, (Cagnon *et al.*, Protein Engineering (1991) 4(7):843)); the promoter of the gene of bacteriophage T7 encoding RNA polymerase, that is functional in a number of *E. coli* strains expressing T7 polymerase (described in U.S. Patent No. 4,952,496); OspA lipidation signal peptide ; and RlpB lipidation signal peptide (Takase *et al.*, J. Bact. (1987) 169:5692).

The expression cassette is typically part of an expression vector, which is selected for its ability to replicate in the chosen expression system. Expression vectors (*e.g.*, plasmids or viral vectors) can be chosen, for example, from those described in Pouwels *et al.* (Cloning Vectors: A Laboratory Manual 1985, Supp. 1987). Suitable expression vectors can be purchased from various commercial sources.

Methods for transforming/transfecting host cells with expression vectors are well-known in the art and depend on the

host system selected as described in Ausubel *et al.*, (Ausubel *et al.*, Current Protocols in Molecular Biology, John Wiley & Sons Inc., 1994).

Upon expression, a recombinant polypeptide of the invention (or a polypeptide derivative) is produced and remains in the intracellular compartment, is secreted/excreted in the extracellular medium or in the periplasmic space, or is embedded in the cellular membrane. The polypeptide is recovered in a substantially purified form from the cell extract or from the supernatant after centrifugation of the recombinant cell culture. Typically, the recombinant polypeptide is purified by antibody-based affinity purification or by other well-known methods that can be readily adapted by a person skilled in the art, such as fusion of the polynucleotide encoding the polypeptide or its derivative to a small affinity binding domain. Antibodies useful for purifying by immunoaffinity the polypeptides of the invention are obtained as described below.

A polynucleotide of the invention can also be useful as a vaccine. There are two major routes, either using a viral or bacterial host as gene delivery vehicle (live vaccine vector) or administering the gene in a free form, *e.g.*, inserted into a plasmid. Therapeutic or prophylactic efficacy of a polynucleotide of the invention is evaluated as described below.

Accordingly, a third aspect of the invention provides (i) a vaccine vector such as a poxvirus, containing a DNA molecule of the invention, placed under the control of elements required for expression; (ii) a composition of matter comprising a vaccine vector of the invention, together with a diluent or carrier; specifically (iii) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a vaccine vector of the invention; (iv) a method for inducing an immune response against *Chlamydia* in a mammal (*e.g.*, a human; alternatively, the method can be used in veterinary applications for treating or preventing *Chlamydia* infection of

animals, *e.g.*, cats or birds), which involves administering to the mammal an immunogenically effective amount of a vaccine vector of the invention to elicit a protective or therapeutic immune response to *Chlamydia* ; and particularly, (v) a method for preventing and/or treating a *Chlamydia* (*e.g.*, *C. trachomatis, C. psittaci, C. pneumonia, C. pecorum*) infection, which involves administering a prophylactic or therapeutic amount of a vaccine vector of the invention to an infected individual. Additionally, the third aspect of the invention encompasses the use of a vaccine vector of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection.

As used herein, a vaccine vector expresses one or several polypeptides or derivatives of the invention. The vaccine vector may express additionally a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12), that enhances the immune response (adjuvant effect). It is understood that each of the components to be expressed is placed under the control of elements required for expression in a mammalian cell.

Consistent with the third aspect of the invention is a composition comprising several vaccine vectors, each of them capable of expressing a polypeptide or derivative of the invention. A composition may also comprise a vaccine vector capable of expressing an additional *Chlamydia* antigen, or a subunit, fragment, homolog, mutant, or derivative thereof, optionally together with a cytokine such as IL-2 or IL-12.

Vaccination methods for treating or preventing infection in a mammal comprises use of a vaccine vector of the invention to be administered by any conventional route, particularly to a mucosal (*e.g.*, ocular, intranasal, oral, gastric, pulmonary, intestinal, rectal, vaginal, or urinary tract) surface or *via* the parenteral (*e.g.*, subcutaneous, intradermal, intramuscular, intravenous, or intraperitoneal) route. Preferred routes depend upon the choice of the vaccine vector. Treatment may be

effected in a single dose or repeated at intervals. The appropriate dosage depends on various parameters understood by skilled artisans such as the vaccine vector itself, the route of administration or the condition of the mammal to be vaccinated (weight, age and the like).

Live vaccine vectors available in the art include viral vectors such as adenoviruses and poxviruses as well as bacterial vectors, *e.g.*, *Shigella*, *Salmonella*, *Vibrio cholerae*, *Lactobacillus*, Bacille bilié de Calmette-Guérin (BCG), and *Streptococcus*.

An example of an adenovirus vector, as well as a method for constructing an adenovirus vector capable of expressing a DNA molecule of the invention, are described in U.S. Patent No. 4,920,209. Poxvirus vectors include vaccinia and canary pox virus, described in U.S. Patent No. 4,722,848 and U.S. Patent No. 5,364,773, respectively. (Also see, *e.g.*, Tartaglia *et al.*, Virology (1992) 188:217) for a description of a vaccinia virus vector and Taylor *et al*, Vaccine (1995) 13:539 for a reference of a canary pox.) Poxvirus vectors capable of expressing a polynucleotide of the invention are obtained by homologous recombination as described in Kieny *et al.*, Nature (1984) 312:163 so that the polynucleotide of the invention is inserted in the viral genome under appropriate conditions for expression in mammalian cells. Generally, the dose of vaccine viral vector, for therapeutic or prophylactic use, can be of from about $1x10^4$ to about $1x10^{11}$, advantageously from about $1x10^7$ to about $1x10^{10}$, preferably of from about $1x10^7$ to about $1x10^9$ plaque-forming units per kilogram. Preferably, viral vectors are administered parenterally; for example, in 3 doses, 4 weeks apart. It is preferable to avoid adding a chemical adjuvant to a composition containing a viral vector of the invention and thereby minimizing the immune response to the viral vector itself.

Non-toxicogenic *Vibrio cholerae* mutant strains that are useful as a live oral vaccine are known. Mekalanos *et al.*, Nature (1983) 306:551 and U.S. Patent No. 4,882,278 describe strains which have a substantial amount of the coding sequence of each of the two *ctxA* alleles deleted so that no functional *cholerae* toxin is produced. WO 92/11354 describes a strain in which the *irgA* locus is inactivated by mutation; this mutation can be combined in a single strain with *ctxA* mutations. WO 94/01533 describes a deletion mutant lacking functional *ctxA* and *attRS1* DNA sequences. These mutant strains are genetically engineered to express heterologous antigens, as described in WO 94/19482. An effective vaccine dose of a *Vibrio cholerae* strain capable of expressing a polypeptide or polypeptide derivative encoded by a DNA molecule of the invention contains about $1x10^5$ to about $1x10^9$, preferably about $1x10^6$ to about $1x10^8$, viable bacteria in a volume appropriate for the selected route of administration. Preferred routes of administration include all mucosal routes; most preferably, these vectors are administered intranasally or orally.

Attenuated *Salmonella typhimurium* strains, genetically engineered for recombinant expression of heterologous antigens or not, and their use as oral vaccines are described in Nakayama *et al.* (Bio/Technology (1988) 6:693) and WO 92/11361. Preferred routes of administration include all mucosal routes; most preferably, these vectors are administered intranasally or orally.

Other bacterial strains used as vaccine vectors in the context of the present invention are described for *Shigella flexneri* in High *et al.*, EMBO (1992) 11:1991 and Sizemore *et al.*, Science (1995) 270:299; for *Streptococcus gordonii* in Medaglini *et al.*, Proc. Natl. Acad. Sci. USA (1995) 92:6868; and for Bacille Calmette Guerin in Flynn J.L., Cell. Mol. Biol. (1994) 40 (suppl. I):31, WO 88/06626, WO 90/00594, WO 91/13157, WO 92/01796, and WO 92/21376.

In bacterial vectors, the polynucleotide of the invention is inserted into the bacterial genome or remains in a free state as part of a plasmid.

The composition comprising a vaccine bacterial vector of the present invention may further contain an adjuvant. A number of adjuvants are known to those skilled in the art. Preferred adjuvants as provided below.

Accordingly, a fourth aspect of the invention provides (i) a composition of matter comprising a polynucleotide of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a polynucleotide of the invention; (iii) a method for inducing an immune response against *Chlamydia* in a mammal by administration of an immunogenically effective amount of a polynucleotide of the invention to elicit a protective immune response to *Chlamydia*; and particularly, (iv) a method for preventing and/or treating a *Chlamydia* (*e.g., C. trachomatis, C. psittaci, C. pneumoniae, or C. pecorum*) infection, by administering a prophylactic or therapeutic amount of a polynucleotide of the invention to an infected individual. Additionally, the fourth aspect of the invention encompasses the use of a polynucleotide of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection. A preferred use includes the use of a DNA molecule placed under conditions for expression in a mammalian cell, especially in a plasmid that is unable to replicate in mammalian cells and to substantially integrate in a mammalian genome.

Uses of the polynucleotides of the invention include their administration to a mammal as a vaccine, for therapeutic or prophylactic purposes. Such polynucleotides are used in the form of DNA as part of a plasmid that is unable to replicate in a mammalian cell and unable to integrate into the mammalian genome. Typically, such a DNA molecule is placed under the

control of a promoter suitable for expression in a mammalian cell. The promoter functions either ubiquitously or tissue-specifically. Examples of non-tissue specific promoters include the early Cytomegalovirus (CMV) promoter (described in U.S. Patent No. 4,168,062) and the Rous Sarcoma Virus promoter (described in Norton & Coffin, Molec. Cell Biol. (1985) 5:281). An example of a tissue-specific promoter is the desmin promoter which drives expression in muscle cells (Li *et al.*, Gene (1989) 78:243, Li & Paulin, J. Biol. Chem. (1991) 266:6562 and Li & Paulin, J. Biol. Chem. (1993) 268:10403). Use of promoters is well-known to those skilled in the art. Useful vectors are described in numerous publications, specifically WO 94/21797 and Hartikka *et al.*, Human Gene Therapy (1996) 7:1205.

Polynucleotides of the invention which are used as vaccines encode either a precursor or a mature form of the corresponding polypeptide. In the precursor form, the signal peptide is either homologous or heterologous. In the latter case, a eucaryotic leader sequence such as the leader sequence of the tissue-type plasminogen factor (tPA) is preferred.

As used herein, a composition of the invention contains one or several polynucleotides with optionally at least one additional polynucleotide encoding another *Chlamydia* antigen such as urease subunit A, B, or both, or a fragment, derivative, mutant, or analog thereof. The composition may also contain an additional polynucleotide encoding a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12) so that the immune response is enhanced. These additional polynucleotides are placed under appropriate control for expression. Advantageously, DNA molecules of the invention and/or additional DNA molecules to be included in the same composition, are present in the same plasmid.

Standard techniques of molecular biology for preparing and purifying polynucleotides are used in the preparation of polynucleotide therapeutics of the invention. For use as a

vaccine, a polynucleotide of the invention is formulated according to various methods outlined below.

One method utilizes the polynucleotide in a naked form, free of any delivery vehicles. Such a polynucleotide is simply diluted in a physiologically acceptable solution such as sterile saline or sterile buffered saline, with or without a carrier. When present, the carrier preferably is isotonic, hypotonic, or weakly hypertonic, and has a relatively low ionic strength, such as provided by a sucrose solution, *e.g.*, a solution containing 20% sucrose.

An alternative method utilizes the polynucleotide in association with agents that assist in cellular uptake. Examples of such agents are (i) chemicals that modify cellular permeability, such as bupivacaine (see, *e.g.*, WO 94/16737), (ii) liposomes for encapsulation of the polynucleotide, or (iii) cationic lipids or silica, gold, or tungsten microparticles which associate themselves with the polynucleotides.

Anionic and neutral liposomes are well-known in the art (see, *e.g.*, Liposomes: A Practical Approach, RPC New Ed, IRL press (1990), for a detailed description of methods for making liposomes) and are useful for delivering a large range of products, including polynucleotides.

Cationic lipids are also known in the art and are commonly used for gene delivery. Such lipids include Lipofectin™ also known as DOTMA (N-[1-(2,3-dioleyloxy)propyl]-N,N,N-trimethylammonium chloride), DOTAP (1,2-bis(oleyloxy)-3-(trimethylammonio)propane), DDAB (dimethyldioctadecylammonium bromide), DOGS (dioctadecylamidologlycyl spermine) and cholesterol derivatives such as DC-Chol (3 beta-(N-(N',N'-dimethyl aminomethane)-carbamoyl) cholesterol). A description of these cationic lipids can be found in EP 187,702, WO 90/11092, U.S. Patent No. 5,283,185, WO 91/15501, WO 95/26356, and U.S. Patent No. 5,527,928. Cationic lipids for

gene delivery are preferably used in association with a neutral lipid such as DOPE (dioleyl phosphatidylethanolamine), as described in WO 90/11092 as an example.

Formulation containing cationic liposomes may optionally contain other transfection-facilitating compounds. A number of them are described in WO 93/18759, WO 93/19768, WO 94/25608, and WO 95/02397. They include spermine derivatives useful for facilitating the transport of DNA through the nuclear membrane (see, for example, WO 93/18759) and membrane-permeabilizing compounds such as GALA, Gramicidine S, and cationic bile salts (see, for example, WO 93/19768).

Gold or tungsten microparticles are used for gene delivery, as described in WO 91/00359, WO 93/17706, and Tang *et al*. Nature (1992) 356:152. The microparticle-coated polynucleotide is injected *via* intradermal or intraepidermal routes using a needleless injection device ("gene gun"), such as those described in U.S. Patent No. 4,945,050, U.S. Patent No. 5,015,580, and WO 94/24263.

The amount of DNA to be used in a vaccine recipient depends, *e.g.*, on the strength of the promoter used in the DNA construct, the immunogenicity of the expressed gene product, the condition of the mammal intended for administration (*e.g.*, the weight, age, and general health of the mammal), the mode of administration, and the type of formulation. In general, a therapeutically or prophylactically effective dose from about 1 μg to about 1 mg, preferably, from about 10 μg to about 800 μg and, more preferably, from about 25 μg to about 250 μg, can be administered to human adults. The administration can be achieved in a single dose or repeated at intervals.

The route of administration is any conventional route used in the vaccine field. As general guidance, a polynucleotide of the invention is administered *via* a mucosal surface, *e.g.*, an ocular, intranasal, pulmonary, oral, intestinal, rectal, vaginal, and urinary tract surface; or *via* a

parenteral route, *e.g.*, by an intravenous, subcutaneous, intraperitoneal, intradermal, intraepidermal, or intramuscular route. The choice of administration route depends on the formulation that is selected. A polynucleotide formulated in association with bupivacaine is advantageously administered into muscles. When a neutral or anionic liposome or a cationic lipid, such as DOTMA or DC-Chol, is used, the formulation can be advantageously injected *via* intravenous, intranasal (aerosolization), intramuscular, intradermal, and subcutaneous routes. A polynucleotide in a naked form can advantageously be administered *via* the intramuscular, intradermal, or subcutaneous routes.

Although not absolutely required, such a composition can also contain an adjuvant. If so, a systemic adjuvant that does not require concomitant administration in order to exhibit an adjuvant effect is preferable such as, *e.g.*, QS21, which is described in U.S. Patent No. 5,057,546.

The sequence information provided in the present application enables the design of specific nucleotide probes and primers that are used for diagnostic purposes. Accordingly, a fifth aspect of the invention provides a nucleotide probe or primer having a sequence found in or derived by degeneracy of the genetic code from a sequence shown in any one of SEQ ID Nos: 1 to 13.

The term "probe" as used in the present application refers to DNA (preferably single stranded) or RNA molecules (or modifications or combinations thereof) that hybridize under the stringent conditions, as defined above, to nucleic acid molecules having SEQ ID Nos: 1 to 13 or to sequences homologous to SEQ ID Nos: 1 to 13, or to their complementary or anti-sense sequences. Generally, probes are significantly shorter than full-length sequences. Such probes contain from about 5 to about 100, preferably from about 10 to about 80, nucleotides. In particular, probes have sequences that are at least 75%,

preferably at least 85%, more preferably 95% homologous to a portion of any of SEQ ID Nos: 1 to 13 or that are complementary to such sequences. Probes may contain modified bases such as inosine, methyl-5-deoxycytidine, deoxyuridine, dimethylamino-5-deoxyuridine, or diamino-2, 6-purine. Sugar or phosphate residues may also be modified or substituted. For example, a deoxyribose residue may be replaced by a polyamide (Nielsen *et al.*, Science (1991) 254:1497) and phosphate residues may be replaced by ester groups such as diphosphate, alkyl, arylphosphonate and phosphorothioate esters. In addition, the 2'-hydroxyl group on ribonucleotides may be modified by including such groups as alkyl groups.

Probes of the invention are used in diagnostic tests, as capture or detection probes. Such capture probes are conventionally immobilized on a solid support, directly or indirectly, by covalent means or by passive adsorption. A detection probe is labelled by a detection marker selected from: radioactive isotopes, enzymes such as peroxidase, alkaline phosphatase, and enzymes able to hydrolyze a chromogenic, fluorogenic, or luminescent substrate, compounds that are chromogenic, fluorogenic, or luminescent, nucleotide base analogs, and biotin.

Probes of the invention are used in any conventional hybridization technique, such as dot blot (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual (1982) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York), Southern blot (Southern, J. Mol. Biol. (1975) 98:503), northern blot (identical to Southern blot with the exception that RNA is used as a target), or the sandwich technique (Dunn *et al.*, Cell (1977) 12:23). The latter technique involves the use of a specific capture probe and/or a specific detection probe with nucleotide sequences that at least partially differ from each other.

A primer is a probe of usually about 10 to about 40 nucleotides that is used to initiate enzymatic polymerization of DNA in an amplification process (*e.g.*, PCR), in an elongation process, or in a reverse transcription method. Primers used in diagnostic methods involving PCR are labeled by methods known in the art.

As described herein, the invention also encompasses (i) a reagent comprising a probe of the invention for detecting and/or identifying the presence of *Chlamydia* in a biological material; (ii) a method for detecting and/or identifying the presence of *Chlamydia* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA or RNA is extracted from the material and denatured, and (c) exposed to a probe of the invention, for example, a capture, detection probe or both, under stringent hybridization conditions, such that hybridization is detected; and (iii) a method for detecting and/or identifying the presence of *Chlamydia* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA is extracted therefrom, (c) the extracted DNA is primed with at least one, and preferably two, primers of the invention and amplified by polymerase chain reaction, and (d) the amplified DNA fragment is produced.

It is apparent that disclosure of polynucleotide sequences of SEQ ID Nos: 1 to 13, their homolog, and partial sequences of either enable their corresponding amino acid sequences. Accordingly, a sixth aspect of the invention features a substantially purified polypeptide or polypeptide derivative having an amino acid sequence encoded by a polynucleotide of the invention.

A "substantially purified polypeptide" as used herein is defined as a polypeptide that is separated from the environment in which it naturally occurs and/or that is free of the majority of the polypeptides that are present in the environment in which

it was synthesized. For example, a substantially purified polypeptide is free from cytoplasmic polypeptides. Those skilled in the art would readily understand that the polypeptides of the invention may be purified from a natural source, *i.e.*, a *Chlamydia* strain, or produced by recombinant means.

Consistent with the sixth aspect of the invention are polypeptides, homologs or fragments which are modified or treated to enhance their immunogenicity in the target animal, in whom the polypeptide, homolog or fragments are intended to confer protection against Chlamydia. Such modifications or treatments include: amino acid substitutions with an amino acid derivative such as 3-methyhistidine, 4-hydroxyproline, 5-hydroxylysine etc., modifications or deletions which are carried out after preparation of the polypeptide, homolog or fragment, such as the modification of free amino, carboxyl or hydroxyl side groups of the amino acids.

Identification of homologous polypeptides or polypeptide derivatives encoded by polynucleotides of the invention which have specific antigenicity is achieved by screening for cross-reactivity with an antiserum raised against the polypeptide of reference having an amino acid sequence of any one of SEQ ID Nos: 14 to 26. The procedure is as follows: a monospecific hyperimmune antiserum is raised against a purified reference polypeptide, a fusion polypeptide (for example, an expression product of MBP, GST, or His-tag systems), or a synthetic peptide predicted to be antigenic. Where an antiserum is raised against a fusion polypeptide, two different fusion systems are employed. Specific antigenicity can be determined according to a number of methods, including Western blot (Towbin *et al.*, Proc. Natl. Acad. Sci. USA (1979) 76:4350), dot blot, and ELISA, as described below.

In a Western blot assay, the product to be screened, either as a purified preparation or a total *E. coli* extract, is

submitted to SDS-Page electrophoresis as described by Laemmli (Nature (1970) 227:680). After transfer to a nitrocellulose membrane, the material is further incubated with the monospecific hyperimmune antiserum diluted in the range of dilutions from about 1:5 to about 1:5000, preferably from about 1:100 to about 1:500. Specific antigenicity is shown once a band corresponding to the product exhibits reactivity at any of the dilutions in the above range.

In an ELISA assay, the product to be screened is preferably used as the coating antigen. A purified preparation is preferred, although a whole cell extract can also be used. Briefly, about 100 µl of a preparation at about 10 µg protein/ml are distributed into wells of a 96-well polycarbonate ELISA plate. The plate is incubated for 2 hours at 37°C then overnight at 4°C. The plate is washed with phosphate buffer saline (PBS) containing 0.05% Tween 20 (PBS/Tween buffer). The wells are saturated with 250 µl PBS containing 1% bovine serum albumin (BSA) to prevent non-specific antibody binding. After a 1 hour incubation at 37°C, the plate is washed with PBS/Tween buffer. The antiserum is serially diluted in PBS/Tween buffer containing 0.5% BSA. 100 µl of dilutions are added per well. The plate is incubated for 90 minutes at 37°C, washed and evaluated according to standard procedures. For example, a goat anti-rabbit peroxidase conjugate is added to the wells when specific antibodies were raised in rabbits. Incubation is carried out for 90 minutes at 37°C and the plate is washed. The reaction is developed with the appropriate substrate and the reaction is measured by colorimetry (absorbance measured spectrophotometrically). Under the above experimental conditions, a positive reaction is shown by O.D. values greater than a non-immune control serum.

In a dot blot assay, a purified product is preferred, although a whole cell extract can also be used. Briefly, a solution of the product at about 100 µg/ml is serially two-fold

diluted in 50 mM Tris-HCl (pH 7.5). 100 µl of each dilution are applied to a nitrocellulose membrane 0.45 µm set in a 96-well dot blot apparatus (Biorad). The buffer is removed by applying vacuum to the system. Wells are washed by addition of 50 mM Tris-HCl (pH 7.5) and the membrane is air-dried. The membrane is saturated in blocking buffer (50 mM Tris-HCl (pH 7.5) 0.15 M NaCl, 10 g/L skim milk) and incubated with an antiserum dilution from about 1:50 to about 1:5000, preferably about 1:500. The reaction is revealed according to standard procedures. For example, a goat anti-rabbit peroxidase conjugate is added to the wells when rabbit antibodies are used. Incubation is carried out 90 minutes at 37°C and the blot is washed. The reaction is developed with the appropriate substrate and stopped. The reaction is measured visually by the appearance of a colored spot, *e.g.*, by colorimetry. Under the above experimental conditions, a positive reaction is shown once a colored spot is associated with a dilution of at least about 1:5, preferably of at least about 1:500.

Therapeutic or prophylactic efficacy of a polypeptide or derivative of the invention can be evaluated as described below. A seventh aspect of the invention provides (i) a composition of matter comprising a polypeptide of the invention together with a diluent or carrier; specifically (ii) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a polypeptide of the invention; (iii) a method for inducing an immune response against *Chlamydia* in a mammal, by administering to the mammal an immunogenically effective amount of a polypeptide of the invention to elicit a protective immune response to *Chlamydia*; and particularly, (iv) a method for preventing and/or treating a *Chlamydia* (*e.g.*, *C. trachomatis*. *C. psittaci*, *C. pneumoniae*. or *C. pecorum*) infection, by administering a prophylactic or therapeutic amount of a polypeptide of the invention to an infected individual. Additionally, the seventh aspect of the invention encompasses

the use of a polypeptide of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection.

As used herein, the immunogenic compositions of the invention are administered by conventional routes known the vaccine field, in particular to a mucosal (*e.g.*, ocular, intranasal, pulmonary, oral, gastric, intestinal, rectal, vaginal, or urinary tract) surface or *via* the parenteral (*e.g.*, subcutaneous, intradermal, intramuscular, intravenous, or intraperitoneal) route. The choice of administration route depends upon a number of parameters, such as the adjuvant associated with the polypeptide. If a mucosal adjuvant is used, the intranasal or oral route is preferred. If a lipid formulation or an aluminum compound is used, the parenteral route is preferred with the sub-cutaneous or intramuscular route being most preferred. The choice also depends upon the nature of the vaccine agent. For example, a polypeptide of the invention fused to CTB or LTB is best administered to a mucosal surface.

As used herein, the composition of the invention contains one or several polypeptides or derivatives of the invention. The composition optionally contains at least one additional *Chlamydia* antigen, or a subunit, fragment, homolog, mutant, or derivative thereof.

For use in a composition of the invention, a polypeptide or derivative thereof is formulated into or with liposomes, preferably neutral or anionic liposomes, microspheres, ISCOMS, or virus-like-particles (VLPs) to facilitate delivery and/or enhance the immune response. These compounds are readily available to one skilled in the art; for example, see Liposomes: A Practical Approach, RPC New Ed, IRL press (1990).

Adjuvants other than liposomes and the like are also used and are known in the art. Adjuvants may protect the antigen from rapid dispersal by sequestering it in a local deposit, or they may contain substances that stimulate the host to secrete

factors that are chemotactic for macrophages and other components of the immune system. An appropriate selection can conventionally be made by those skilled in the art, for example, from those described below (see the eleventh aspect of the invention).

Treatment is achieved in a single dose or repeated as necessary at intervals, as can be determined readily by one skilled in the art. For example, a priming dose is followed by three booster doses at weekly or monthly intervals. An appropriate dose depends on various parameters including the recipient (*e.g.*, adult or infant), the particular vaccine antigen, the route and frequency of administration, the presence/absence or type of adjuvant, and the desired effect (*e.g.*, protection and/or treatment), as can be determined by one skilled in the art. In general, a vaccine antigen of the invention is administered by a mucosal route in an amount from about 10 μg to about 500 mg, preferably from about 1 mg to about 200 mg. For the parenteral route of administration, the dose usually does not exceed about 1 mg, preferably about 100 μg.

When used as vaccine agents, polynucleotides and polypeptides of the invention may be used sequentially as part of a multistep immunization process. For example, a mammal is initially primed with a vaccine vector of the invention such as a pox virus, *e.g.*, *via* the parenteral route, and then boosted twice with the polypeptide encoded by the vaccine vector, *e.g.*, *via* the mucosal route. In another example, liposomes associated with a polypeptide or derivative of the invention is also used for priming, with boosting being carried out mucosally using a soluble polypeptide or derivative of the invention in combination with a mucosal adjuvant (*e.g.*, LT).

A polypeptide derivative of the invention is also used in accordance with the seventh aspect as a diagnostic reagent for detecting the presence of anti-*Chlamydia* antibodies, *e.g.*, in a blood sample. Such polypeptides are about 5 to about 80,

preferably about 10 to about 50 amino acids in length. They are either labeled or unlabeled, depending upon the diagnostic method. Diagnostic methods involving such a reagent are described below.

Upon expression of a DNA molecule of the invention, a polypeptide or polypeptide derivative is produced and purified using known laboratory techniques. As described above, the polypeptide or polypeptide derivative may be produced as a fusion protein containing a fused tail that facilitates purification. The fusion product is used to immunize a small mammal, *e.g.*, a mouse or a rabbit, in order to raise antibodies against the polypeptide or polypeptide derivative (monospecific antibodies). Accordingly, an eighth aspect of the invention provides a monospecific antibody that binds to a polypeptide or polypeptide derivative of the invention.

By "monospecific antibody" is meant an antibody that is capable of reacting with a unique naturally-occurring *Chlamydia* polypeptide. An antibody of the invention is either polyclonal or monoclonal. Monospecific antibodies may be recombinant, *e.g.*, chimeric (*e.g.*, constituted by a variable region of murine origin associated with a human constant region), humanized (a human immunoglobulin constant backbone together with hypervariable region of animal, *e.g.*, murine, origin), and/or single chain. Both polyclonal and monospecific antibodies may also be in the form of immunoglobulin fragments, *e.g.*, F(ab)'2 or Fab fragments. The antibodies of the invention are of any isotype, *e.g.*, IgG or IgA, and polyclonal antibodies are of a single isotype or a mixture of isotypes.

Antibodies against the polypeptides, homologs or fragments of the present invention are generated by immunization of a mammal with a composition comprising said polypeptide, homolog or fragment. Scu antibodies may be polyclonal or monoclonal. Methods to produce polyclonal or monoclonal antibodies are well known in the art. For a review, see

"Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory, Eds. E. Harlow and D. Lane (1988), and D.E. Yelton et al., 1981. Ann. Rev. Biochem. 50:657-680. For monoclonal antibodies, see Kohler and Milstein (1975) Nature. 256:495-497.

The antibodies of the invention, which are raised to a polypeptide or polypeptide derivative of the invention, are produced and identified using standard immunological assays, *e.g.*, Western blot analysis, dot blot assay, or ELISA (see, *e.g.*, Coligan *et al.*, Current Protocols in Immunology (1994) John Wiley & Sons, Inc., New York, NY). The antibodies are used in diagnostic methods to detect the presence of a *Chlamydia* antigen in a sample, such as a biological sample. The antibodies are also used in affinity chromatography for purifying a polypeptide or polypeptide derivative of the invention. As is discussed further below, such antibodies may be used in prophylactic and therapeutic passive immunization methods.

Accordingly, a ninth aspect of the invention provides (i) a reagent for detecting the presence of *Chlamydia* in a biological sample that contains an antibody, polypeptide, or polypeptide derivative of the invention; and (ii) a diagnostic method for detecting the presence of *Chlamydia* in a biological sample, by contacting the biological sample with an antibody, a polypeptide, or a polypeptide derivative of the invention, such that an immune complex is formed, and by detecting such complex to indicate the presence of *Chlamydia* in the sample or the organism from which the sample is derived.

Those skilled in the art will readily understand that the immune complex is formed between a component of the sample and the antibody, polypeptide, or polypeptide derivative, whichever is used, and that any unbound material is removed prior to detecting the complex. It is understood that a polypeptide reagent is useful for detecting the presence of anti-*Chlamydia* antibodies in a sample, *e.g.*, a blood sample, while an antibody

of the invention is used for screening a sample, such as a gastric extract or biopsy, for the presence of *Chlamydia* polypeptides.

For diagnostic applications, the reagent (*i.e.*, the antibody, polypeptide, or polypeptide derivative of the invention) is either in a free state or immobilized on a solid support, such as a tube, a bead, or any other conventional support used in the field. Immobilization is achieved using direct or indirect means. Direct means include passive adsorption (non-covalent binding) or covalent binding between the support and the reagent. By "indirect means" is meant that an anti-reagent compound that interacts with a reagent is first attached to the solid support. For example, if a polypeptide reagent is used, an antibody that binds to it can serve as an anti-reagent, provided that it binds to an epitope that is not involved in the recognition of antibodies in biological samples. Indirect means may also employ a ligand-receptor system, for example, where a molecule such as a vitamin is grafted onto the polypeptide reagent and the corresponding receptor immobilized on the solid phase. This is illustrated by the biotin-streptavidin system. Alternatively, a peptide tail is added chemically or by genetic engineering to the reagent and the grafted or fused product immobilized by passive adsorption or covalent linkage of the peptide tail.

Such diagnostic agents may be included in a kit which also comprises instructions for use. The reagent is labeled with a detection means which allows for the detection of the reagent when it is bound to its target. The detection means may be a fluorescent agent such as fluorescein isocyanate or fluorescein isothiocyanate, or an enzyme such as horse radish peroxidase or luciferase or alkaline phosphatase, or a radioactive element such as ^{125}I or ^{51}Cr.

Accordingly, a tenth aspect of the invention provides a process for purifying, from a biological sample, a polypeptide

or polypeptide derivative of the invention, which involves carrying out antibody-based affinity chromatography with the biological sample, wherein the antibody is a monospecific antibody of the invention.

For use in a purification process of the invention, the antibody is either polyclonal or monospecific, and preferably is of the IgG type. Purified IgGs is prepared from an antiserum using standard methods (see, *e.g.*, Coligan *et al.*, Current Protocols in Immunology (1994) John Wiley & Sons, Inc., New York, NY). Conventional chromatography supports, as well as standard methods for grafting antibodies, are described in, *e.g.*, Antibodies: A Laboratory Manual, D. Lane, E. Harlow, Eds. (1988) and outlined below.

Briefly, a biological sample, such as a *C. pneumoniae* extract preferably in a buffer solution, is applied to a chromatography material, preferably equilibrated with the buffer used to dilute the biological sample so that the polypeptide or polypeptide derivative of the invention (*i.e.*, the antigen) is allowed to adsorb onto the material. The chromatography material, such as a gel or a resin coupled to an antibody of the invention, is in either a batch form or a column. The unbound components are washed off and the antigen is then eluted with an appropriate elution buffer, such as a glycine buffer or a buffer containing a chaotropic agent, *e.g.*, guanidine HCl, or high salt concentration (*e.g.*, 3 M $MgCl_2$). Eluted fractions are recovered and the presence of the antigen is detected, *e.g.*, by measuring the absorbance at 280 nm.

An eleventh aspect of the invention provides (i) a composition of matter comprising a monospecific antibody of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a monospecific antibody of the invention, and (iii) a method for treating or preventing a *Chlamydia* (*e.g.*, *C. trachomatis, C. psittaci, C. pneumoniae or*

C. pecorum) infection, by administering a therapeutic or prophylactic amount of a monospecific antibody of the invention to an infected individual. Additionally, the eleventh aspect of the invention encompasses the use of a monospecific antibody of the invention in the preparation of a medicament for treating or preventing *Chlamydia* infection.

The monospecific antibody is either polyclonal or monoclonal, preferably of the IgA isotype (predominantly). In passive immunization, the antibody is administered to a mucosal surface of a mammal, *e.g.*, the gastric mucosa, *e.g.*, orally or intragastrically, advantageously, in the presence of a bicarbonate buffer. Alternatively, systemic administration, not requiring a bicarbonate buffer, is carried out. A monospecific antibody of the invention is administered as a single active component or as a mixture with at least one monospecific antibody specific for a different *Chlamydia* polypeptide. The amount of antibody and the particular regimen used are readily determined by one skilled in the art. For example, daily administration of about 100 to 1,000 mg of antibodies over one week, or three doses per day of about 100 to 1,000 mg of antibodies over two or three days, are effective regimens for most purposes.

Therapeutic or prophylactic efficacy are evaluated using standard methods in the art, *e.g.*, by measuring induction of a mucosal immune response or induction of protective and/or therapeutic immunity, using, *e.g.*, the C. *pneumoniae* mouse model. Those skilled in the art will readily recognize that the *C. pneumoniae* strain of the model may be replaced with another *Chlamydia* strain. For example, the efficacy of DNA molecules and polypeptides from *C. pneumoniae* is preferably evaluated in a mouse model using *C. pneumoniae* strain. Protection is determined by comparing the degree of *Chlamydia* infection to that of a control group. Protection is shown when infection is reduced by comparison to the control group. Such an evaluation

is made for polynucleotides, vaccine vectors, polypeptides and derivatives thereof, as well as antibodies of the invention.

Adjuvants useful in any of the vaccine compositions described above are as follows.

Adjuvants for parenteral administration include aluminum compounds, such as aluminum hydroxide, aluminum phosphate, and aluminum hydroxy phosphate. The antigen is precipitated with, or adsorbed onto, the aluminum compound according to standard protocols. Other adjuvants, such as RIBI (ImmunoChem, Hamilton, MT), are used in parenteral administration.

Adjuvants for mucosal administration include bacterial toxins, *e.g.*, the cholera toxin (CT), the *E. coli* heat-labile toxin (LT), the *Clostridium difficile* toxin A and the *pertussis* toxin (PT), or combinations, subunits, toxoids, or mutants thereof such as a purified preparation of native cholera toxin subunit B (CTB). Fragments, homologs, derivatives, and fusions to any of these toxins are also suitable, provided that they retain adjuvant activity. Preferably, a mutant having reduced toxicity is used. Suitable mutants are described, *e.g.*, in WO 95/17211 (Arg-7-Lys CT mutant), WO 96/06627 (Arg-192-Gly LT mutant), and WO 95/34323 (Arg-9-Lys and Glu-129-Gly PT mutant). Additional LT mutants that are used in the methods and compositions of the invention include, *e.g.*, Ser-63-Lys, Ala-69-Gly, Glu-110-Asp, and Glu-112-Asp mutants. Other adjuvants, such as a bacterial monophosphoryl lipid A (MPLA) of, *e.g.*, *E. coli*, *Salmonella minnesota*, *Salmonella typhimurium*, or *Shigella flexneri*; saponins, or polylactide glycolide (PLGA) microspheres, are also be used in mucosal administration.

Adjuvants useful for both mucosal and parenteral administrations include polyphosphazene (WO 95/02415), DC-chol (3 b-(N-(N',N'-dimethyl aminomethane)-carbamoyl) cholesterol; U.S. Patent No. 5,283,185 and WO 96/14831) and QS-21 (WO 88/09336).

Any pharmaceutical composition of the invention containing a polynucleotide, a polypeptide, a polypeptide derivative, or an antibody of the invention, is manufactured in a conventional manner. In particular, it is formulated with a pharmaceutically acceptable diluent or carrier, *e.g.*, water or a saline solution such as phosphate buffer saline. In general, a diluent or carrier is selected on the basis of the mode and route of administration, and standard pharmaceutical practice. Suitable pharmaceutical carriers or diluents, as well as pharmaceutical necessities for their use in pharmaceutical formulations, are described in *Remington's Pharmaceutical Sciences*, a standard reference text in this field and in the USP/NF.

The invention also includes methods in which *Chlamydia* infection are treated by oral administration of a *Chlamydia* polypeptide of the invention and a mucosal adjuvant, in combination with an antibiotic, an antacid, sucralfate, or a combination thereof. Examples of such compounds that can be administered with the vaccine antigen and the adjuvant are antibiotics, including, *e.g.*, macrolides, tetracyclines, and derivatives thereof (specific examples of antibiotics that can be used include azithromycin or doxicyclin or immunomodulators such as cytokines or steroids). In addition, compounds containing more than one of the above-listed components coupled together, are used. The invention also includes compositions for carrying out these methods, *i.e.*, compositions containing a *Chlamydia* antigen (or antigens) of the invention, an adjuvant, and one or more of the above-listed compounds, in a pharmaceutically acceptable carrier or diluent.

Amounts of the above-listed compounds used in the methods and compositions of the invention are readily determined by one skilled in the art. Treatment/immunization schedules are also known and readily designed by one skilled in the art. For example, the non-vaccine components can be administered on days

1-14, and the vaccine antigen + adjuvant can be administered on days 7, 14, 21, and 28.

CLAIMS:

1. A nucleic acid molecule comprising a nucleic acid sequence which encodes a polypeptide selected from any of:

(a) SEQ ID Nos: 15 to 26;

(b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and

(c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

2. A nucleic acid molecule comprising a nucleic acid sequence selected from any of:

(a) SEQ ID Nos: 2 to 13;

(b) a sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 2 to 13;

(c) a sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (a) and (b); and

(d) a sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to any one of the polypeptides encoded by SEQ ID Nos: 2 to 13.

3. A nucleic acid molecule comprising a nucleic acid sequence which is anti-sense to the nucleic acid molecule of claim 1 or 2.

4. A nucleic acid molecule comprising a nucleic acid sequence which encodes a fusion protein, said fusion protein comprising a polypeptide encoded by a nucleic acid molecule according to claim 1 and a second polypeptide.

5. The nucleic acid molecule of claim 4 wherein the second polypeptide is a heterologous signal peptide.

6. The nucleic acid molecule of claim 4 wherein the second polypeptide has adjuvant activity.

7. A nucleic acid molecule according to any one of claims 1 to 6, operatively linked to one or more expression control sequences.

8. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any of:

(i) SEQ ID Nos: 1 to 13;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iii) a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (i) and (ii);

(iv) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(v) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(vi) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vii) a nucleic acid sequence which encodes a polypeptide as defined in (v) or an immunogenic fragment as defined in (vi) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (v) or the corresponding fragment of (vi);

wherein each first nucleic acid is capable of being expressed and wherein the vaccine optionally comprises a second nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

9. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed and wherein the vaccine optionally comprises a second nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune response to the first polypeptide.

10. The vaccine of claim 9 wherein the second polypeptide is a heterologous signal peptide.

11. The vaccine of claim 9 wherein the second polypeptide has adjuvant activity.

12. The vaccine of any one of claims 8 to 11 wherein wherein each first nucleic acid is operatively linked to one or more expression control sequences.

13. A vaccine comprising at least one first nucleic acid according to any one of claims 1, 2, and 4 to 7 and a vaccine vector wherein each first nucleic acid is expressed as a polypeptide, the vaccine optionally comprising a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by said first nucleic acid.

14. The vaccine of any one of claims 8 to 13 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

15. A pharmaceutical composition comprising a nucleic acid according to any one of claims 1 to 7 and a pharmaceutically acceptable carrier.

16. A pharmaceutical composition comprising a vaccine according to any one of claims 8 to 14 and a pharmaceutically acceptable carrier.

17. A unicellular host transformed with the nucleic acid molecule of claim 7.

18. An isolated nucleic acid probe of 5 to 100 nucleotides which hybridizes under stringent conditions to any one of nucleic acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

19. An isolated primer of 10 to 40 nucleotides which hybridizes under stringent conditions to any one of nucleic

acid molecules of SEQ ID Nos: 2 to 13, or to a complementary or anti-sense sequence of said nucleic acid molecule.

20. A polypeptide encoded by a nucleic acid sequence according to any one of claims 1, 2 and 4 to 7.

21. A polypeptide comprising an amino acid sequence selected from any of:

(a) SEQ ID Nos: 15 to 26;

(b) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and

(c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

22. A fusion protein comprising a polypeptide of claim 20 or 21 and a second polypeptide.

23. The fusion protein of claim 22 wherein the second polypeptide is a heterologous signal peptide.

24. The fusion protein of claim 22 wherein the second polypeptide has adjuvant activity.

25. A method for producing a polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24, comprising the step of culturing a unicellular host of claim 17.

26. An antibody against the polypeptide of claim 20 or 21, or against a fusion protein of any one of claims 22 to 24.

27. A vaccine comprising at least one first polypeptide selected from any of:

(i) a polypeptide encoded by any one of

SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined in (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v);

wherein the vaccine optionally comprises an additional polypeptide which enhances the immune response to the first polypeptide.

28. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of SEQ ID Nos: 1 to 13;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1 to 13;

(iv) a polypeptide whose sequence is set forth in any one of SEQ ID Nos: 14 to 26;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 14 to 26; and

(vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

wherein the vaccine optionally comprises an additional polypeptide which enhances the immune response to the first polypeptide.

29. The vaccine of claim 28 wherein the second polypeptide is a heterologous signal peptide.

30. The vaccine of claim 28 wherein the second polypeptide has adjuvant activity.

31. A vaccine comprising at least one first polypeptide according to any one of claims 20 to 24, optionally comprising an additional polypeptide which enhances the immune response to the first polypeptide.

32. The vaccine of any one of claims 27 to 31 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

33. A pharmaceutical composition comprising a polypeptide according to any one of claims 20 to 24 and a pharmaceutically acceptable carrier.

34. A pharmaceutical composition comprising a vaccine according to any one of claims 27 to 32 and a pharmaceutically acceptable carrier.

35. A pharmaceutical composition comprising an antibody according to claim 26 and a pharmaceutically acceptable carrier.

36. A method for preventing or treating *Chlamydia* infection using:

(a) the nucleic acid of any one of claims 1 to 7;

(b) the vaccine of any one of claims 8 to 14 and 27 to 32;

(c) the pharmaceutical composition of any one of claims 15, 16 and 33 to 35;

(d) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; or

(e) the antibody of claim 26.

37. A method of detecting *Chlamydia* infection comprising the step of assaying a body fluid of a mammal to be tested, with a component selected from any one of:

(a) the nucleic acid of any one of claims 1 to 7;

(b) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; and

(c) the antibody of claim 26.

38. A diagnostic kit comprising instructions for use and a component selected from any one of:

(a) the nucleic acid of any one of claims 1 to 7;

(b) the polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24; and

(c) the antibody of claim 26.

39. A method for identifying a polypeptide of claim 20 or 21, or a fusion protein of any one of claims 22 to 24 which induces an immune response effective to prevent or lessen the

severity of *Chlamydia* infection in a mammal previously immunized with polypeptide, comprising the steps of:

(a) immunizing a mouse with the polypeptide or fusion protein; and

(b) inoculating the immunized mouse with *Chlamydia*; wherein the polypeptide or fusion protein which prevents or lessens the severity of *Chlamydia* infection in the immunized mouse compared to a non-immunized control mouse is identified.

40. A nucleic acid molecule comprising a nucleic acid sequence which encodes a polypeptide selected from any of:

(a) SEQ ID No: 14;

(b) an immunogenic fragment comprising at least 50 consecutive amino acids from a polypeptide of (a); and

(c) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

41. A nucleic acid molecule comprising a nucleic acid sequence selected from any of:

(a) SEQ ID No: 1;

(b) a sequence which encodes a polypeptide encoded by SEQ ID No: 1;

(c) a sequence comprising at least 38 consecutive nucleotides from SEQ ID No: 1;

(d) a sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1; and

(e) a sequence comprising at least 100 consecutive nucleotides from a nucleic acid sequence of (b).

42. A nucleic acid molecule comprising a nucleic acid sequence which is anti-sense to the nucleic acid molecule of claim 40.

43. A nucleic acid molecule comprising a nucleic acid sequence which encodes a fusion protein, said fusion protein comprising a polypeptide encoded by a nucleic acid molecule according to claim 40 and a second polypeptide.

44. The nucleic acid molecule of claim 43 wherein the second polypeptide is a heterologous signal peptide.

45. The nucleic acid molecule of claim 43 wherein the second polypeptide has adjuvant activity.

46. A nucleic acid molecule according to any one of claims 40 to 45, operatively linked to one or more expression control sequences.

47. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any of:

(i) SEQ ID No: 1;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 1;

(iii) a nucleic acid sequence comprising at least 38 consecutive nucleotides from any one of the nucleic acid sequences of (i) and (ii);

(iv) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1;

(v) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 14;

(vi) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:14; and

(vii) a nucleic acid sequence which encodes a polypeptide as defined in (v) or an immunogenic fragment as defined in (vi) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical

in amino acid sequence to the corresponding polypeptide of (v) or the corresponding fragment of (vi);

wherein each first nucleic acid is capable of being expressed and wherein the vaccine optionally comprises a second nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

48. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by SEQ ID No: 1;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from SEQ ID No: 1;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1;

(iv) a polypeptide whose sequence is set forth in SEQ ID No: 14;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:14; and

(vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed and wherein the vaccine optionally comprises a second nucleic acid encoding and capable of expressing an additional polypeptide which enhances the immune response to the first polypeptide.

49. The vaccine of claim 48 wherein the second polypeptide is a heterologous signal peptide.

50. The vaccine of claim 48 wherein the second polypeptide has adjuvant activity.

51. The vaccine of any one of claims 47 to 50 wherein wherein each first nucleic acid is operatively linked to one or more expression control sequences.

52. A vaccine comprising at least one first nucleic acid according to any one of claims 40, 41, and 43 to 46 and a vaccine vector wherein each first nucleic acid is expressed as a polypeptide, the vaccine optionally comprising a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by said first nucleic acid.

53. The vaccine of any one of claims 47 to 52 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

54. A pharmaceutical composition comprising a nucleic acid according to any one of claims 40 to 46 and a pharmaceutically acceptable carrier.

55. A pharmaceutical composition comprising a vaccine according to any one of claims 47 to 53 and a pharmaceutically acceptable carrier.

56. A unicellular host transformed with the nucleic acid molecule of claim 46.

57. An isolated nucleic acid probe of 5 to 100 nucleotides which are at least 75% similar to the nucleic acid

molecule of SEQ ID No: 1, or to a complementary or anti-sense sequence of said nucleic acid molecule.

58. An isolated primer of 10 to 40 nucleotides which which are at least 75% similar to the nucleic acid molecules of SEQ ID No: 1, or to a complementary or anti-sense sequence of said nucleic acid molecule.

59. A polypeptide encoded by a nucleic acid sequence according to any one of claims 40, 41 and 43 to 46.

60. A polypeptide comprising an amino acid sequence selected from any of:

(d) SEQ ID No: 14;

(e) an immunogenic fragment comprising at least 12 consecutive amino acids from a polypeptide of (a); and

(f) a polypeptide of (a) or (b) which has been modified without loss of immunogenicity, wherein said modified polypeptide is at least 75% identical in amino acid sequence to the corresponding polypeptide of (a) or (b).

61. A fusion protein comprising a polypeptide of claim 59 or 60 and a second polypeptide.

62. The fusion protein of claim 61 wherein the second polypeptide is a heterologous signal peptide.

63. The fusion protein of claim 61 wherein the second polypeptide has adjuvant activity.

64. A method for producing a polypeptide of claim 59 or 60, or a fusion protein of any one of claims 61 to 63, comprising the step of culturing a unicellular host of claim 56.

65. An antibody against the polypeptide of claim 59 or 60, or against a fusion protein of any one of claims 61 to 63.

66. A vaccine comprising at least one first polypeptide selected from any of:

(i) a polypeptide encoded by SEQ ID No: 1;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from SEQ ID No: 1;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1;

(iv) a polypeptide whose sequence is set forth in SEQ ID No: 14;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:14; and

(vi) a polypeptide as defined in (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v);

wherein the vaccine optionally comprises an additional polypeptide which enhances the immune response to the first polypeptide.

67. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide selected from any of:

(i) a polypeptide encoded by SEQ ID No: 1;

(ii) a polypeptide encoded by a nucleic acid sequence comprising at least 38 consecutive nucleotides from SEQ ID No: 1;

(iii) a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1;

(iii) a polypeptide whose sequence is set forth in

SEQ ID No: 14;

(v) an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:14; and

(vi) a polypeptide as defined (iv) or an immunogenic fragment as defined in (v) which has been modified without loss of immunogenicity, wherein said modified polypeptide or fragment is at least 75% identical in amino acid sequence to the corresponding polypeptide of (iv) or the corresponding fragment of (v); and

(b) a second polypeptide;

wherein the vaccine optionally comprises an additional polypeptide which enhances the immune response to the first polypeptide.

68. The vaccine of claim 67 wherein the second polypeptide is a heterologous signal peptide.

69. The vaccine of claim 67 wherein the second polypeptide has adjuvant activity.

70. A vaccine comprising at least one first polypeptide according to any one of claims 59 to 63, optionally comprising an additional polypeptide which enhances the immune response to the first polypeptide.

71. The vaccine of any one of claims 66 to 70 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

72. A pharmaceutical composition comprising a polypeptide according to any one of claims 59 to 63 and a pharmaceutically acceptable carrier.

73. A pharmaceutical composition comprising a vaccine according to any one of claims 66 to 71 and a pharmaceutically acceptable carrier.

74. A pharmaceutical composition comprising an antibody according to claim 65 and a pharmaceutically acceptable carrier.

75. A method for preventing or treating *Chlamydia* infection using:

(f) the nucleic acid of any one of claims 40 to 46;

(g) the vaccine of any one of claims 47 to 53 and 66 to 71;

(h) the pharmaceutical composition of any one of claims 54, 55 and 72 to 74;

(i) the polypeptide of claim 59 or 60, or a fusion protein of any one of claims 61 to 63; or

(j) the antibody of claim 65.

76. A method of detecting *Chlamydia* infection comprising the step of assaying a body fluid of a mammal to be tested, with a component selected from any one of:

(d) the nucleic acid of any one of claims 40 to 46;

(e) the polypeptide of claim 59 or 60, or a fusion protein of any one of claims 61 to 63; and

(f) the antibody of claim 65.

77. A diagnostic kit comprising instructions for use and a component selected from any one of:

(d) the nucleic acid of any one of claims 40 to 46;

(e) the polypeptide of claim 59 or 60, or a fusion protein of any one of claims 61 to 63; and

(f) the antibody of claim 65.

78. A method for identifying a polypeptide of claim 59 or 60, or a fusion protein of any one of claims 61 to 63 which induces an immune response effective to prevent or lessen the severity of *Chlamydia* infection in a mammal previously immunized with polypeptide, comprising the steps of:

(a) immunizing a mouse with the polypeptide or fusion protein; and

(b) inoculating the immunized mouse with *Chlamydia*, wherein the polypeptide or fusion protein which prevents or lessens the severity of *Chlamydia* infection in the immunized mouse compared to a non-immunized control mouse is identified.

<110> Connaught Laboratories Limited

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Gln Leu Asn Glu Glu Ile Leu Thr Ile Thr Ser Lys Ala Lys Gln Arg
                170                 175                 180

cat att tta gtt tcc cat gga gcc ttt ggg tat ttt tgc cgt gat tac   691
His Ile Leu Val Ser His Gly Ala Phe Gly Tyr Phe Cys Arg Asp Tyr
            185                 190                 195

aat ttc tct cag cac act ata gag aaa agc agt cat gtt gag cct tct   739
Asn Phe Ser Gln His Thr Ile Glu Lys Ser Ser His Val Glu Pro Ser
        200                 205                 210

cct aaa gat gtg gct cgc gta ttt cgt gac att gaa cag tac aaa att   787
Pro Lys Asp Val Ala Arg Val Phe Arg Asp Ile Glu Gln Tyr Lys Ile
    215                 220                 225

tct tct gtg att ctt ctc gaa tac tct gga aga cga agt agt gct atg   835
Ser Ser Val Ile Leu Leu Glu Tyr Ser Gly Arg Arg Ser Ser Ala Met
230                 235                 240                 245

ctg gca gat cgt ttc cac atg cat act gtg aat ctc gat ccc tat gcg   883
Leu Ala Asp Arg Phe His Met His Thr Val Asn Leu Asp Pro Tyr Ala
                250                 255                 260

gaa aat gta ctt gta aac tta aaa acc ata gcg acg act ttt tct agt   931
Glu Asn Val Leu Val Asn Leu Lys Thr Ile Ala Thr Thr Phe Ser Ser
            265                 270                 275

tta tgacaatacg aattcttgct gaaggcctag ctttccgtta cggaagcaag        984
Leu

ggaccgaata tcattcatga tgtttctttc tctgtctatg atggcgactt tataggaatc 1044

atagga                                                           1050


<210> 5
<211> 1550
<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (10)..(1416)

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          Met Gly Pro Gly Ser Val Leu Ser Asn His Ser Lys Glu Ala
            1               5                  10
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gga gga atc gct ata aac aat gtc atc att gat ttt agt gaa atc gtt   99
Gly Gly Ile Ala Ile Asn Asn Val Ile Ile Asp Phe Ser Glu Ile Val
 15                  20                  25                  30

cct act aaa gat aat gca aca gta gct cca ccc act ctt aaa tta gta   147
Pro Thr Lys Asp Asn Ala Thr Val Ala Pro Pro Thr Leu Lys Leu Val
                 35                  40                  45

tcg aga act aat gca gat agt aaa gat aag att gat att aca gga act   195
Ser Arg Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp Ile Thr Gly Thr
             50                  55                  60

gtg act ctt cta gat cct aat ggc aac tta tat caa aat tct tat ctt   243
Val Thr Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln Asn Ser Tyr Leu
         65                  70                  75

ggt gaa gac cgc gat atc act ctt ttc aat ata gac aat tct gca agt   291
Gly Glu Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp Asn Ser Ala Ser
     80                  85                  90

ggg gca gtt aca gcc acg aat gtc acc ctt caa ggg aat tta gga gct   339
Gly Ala Val Thr Ala Thr Asn Val Thr Leu Gln Gly Asn Leu Gly Ala
 95                  100                 105                 110

aaa aaa gga tat tta gga acc tgg aat ttg gat cca aat tcc tcg ggt   387
Lys Lys Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro Asn Ser Ser Gly
                115                 120                 125

tca aaa att att cta aaa tgg acc ttt gac aaa tac ctg cgc tgg ccc   435
Ser Lys Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr Leu Arg Trp Pro
            130                 135                 140

tac atc cct aga gac aac cac ttc tac atc aac tct att tgg gga gca   483
Tyr Ile Pro Arg Asp Asn His Phe Tyr Ile Asn Ser Ile Trp Gly Ala
        145                 150                 155

caa aac tct tta gtg act gtg aac caa ggg atc tta ggg aac atg ttg   531
Gln Asn Ser Leu Val Thr Val Asn Gln Gly Ile Leu Gly Asn Met Leu
    160                 165                 170

aac aat gca agg ttt gaa gat cct gct ttc aac aac ttc tgg gct tcg   579
Asn Asn Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn Phe Trp Ala Ser
175                 180                 185                 190

gct ata gga tct ttc ctt agg aaa gaa gta tct cga aat tct gac tca   627
Ala Ile Gly Ser Phe Leu Arg Lys Glu Val Ser Arg Asn Ser Asp Ser
                195                 200                 205

ttc acc tat cat ggc aga ggc tat acc gct gct gtg gat gcc aaa cct   675
Phe Thr Tyr His Gly Arg Gly Tyr Thr Ala Ala Val Asp Ala Lys Pro
            210                 215                 220

cgc caa gaa ttt att tta gga gct gcc ttc agt cag gtt ttt ggt cac   723
Arg Gln Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln Val Phe Gly His
        225                 230                 235
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gcc gag tct gaa tat cac ctt gac aac tat aag cat aaa ggc tca ggt   771
Ala Glu Ser Glu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly
    240                 245                 250

cac tct aca caa gca tct ctt tat gct ggc aat atc ttc tat ttt cct   819
His Ser Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile Phe Tyr Phe Pro
255                 260                 265                 270

gcg ata cgg tct cgg cct att cta ttc caa ggt gtg gcg acc tat ggt   867
Ala Ile Arg Ser Arg Pro Ile Leu Phe Gln Gly Val Ala Thr Tyr Gly
                275                 280                 285

tat atg caa cat gac acc aca acc tac tat cct tct att gaa gaa aaa   915
Tyr Met Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser Ile Glu Glu Lys
            290                 295                 300

aat atg gca aac tgg gat agc att gct tgg tta ttt gat ctg cgt ttc   963
Asn Met Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe Asp Leu Arg Phe
        305                 310                 315

agt gtg gat ctt aaa gaa cct caa cct cac tct aca gca agg ctt acc   1011
Ser Val Asp Leu Lys Glu Pro Gln Pro His Ser Thr Ala Arg Leu Thr
    320                 325                 330

ttc tat aca gaa gct gag tat acc aga att cgc cag gag aaa ttc aca   1059
Phe Tyr Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln Glu Lys Phe Thr
335                 340                 345                 350

gag cta gac tat gat cct aga tct ttc tct gca tgc tct tat gga aac   1107
Glu Leu Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys Ser Tyr Gly Asn
                355                 360                 365

tta gca att cct act gga ttc tct gta gac gga gca tta gct tgg cgt   1155
Leu Ala Ile Pro Thr Gly Phe Ser Val Asp Gly Ala Leu Ala Trp Arg
            370                 375                 380

gag att att cta tat aat aaa gta tca gct gcg tac ctc cct gtg att   1203
Glu Ile Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr Leu Pro Val Ile
        385                 390                 395

ctc agg aat aat cca aaa gcg acc tat gaa gtt ctc tct aca aaa gaa   1251
Leu Arg Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu Ser Thr Lys Glu
    400                 405                 410

aag ggc aac gta gtc aac gtt ctc cct aca aga aac gca gct cgt gca   1299
Lys Gly Asn Val Val Asn Val Leu Pro Thr Arg Asn Ala Ala Arg Ala
415                 420                 425                 430

gag gtg agc tct caa att tat ctt gga agt tac tgg aca ctc tac ggc   1347
Glu Val Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp Thr Leu Tyr Gly
                435                 440                 445

acg tat act att gat gct tca atg aat act tta gtg caa atg gcc aac   1395
Thr Tyr Thr Ile Asp Ala Ser Met Asn Thr Leu Val Gln Met Ala Asn
            450                 455                 460
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gga ggg atc cgg ttt gta ttc tagggtatac aattaaagat tttatgaaat      1446
Gly Gly Ile Arg Phe Val Phe
        465

tgaggatacg gagagagtgg gattcgaacc cacggtacgc gttaacgcac acacgctttc 1506

caagcgtgct ccttaagcca ctcggacatc tctccatatt tata                  1550

<210> 6
<211> 2950
<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (101)..(2866)

<400> 6
aattcttttt aagtgacaag aaattcttgt gctcggcttg ctttcttatt cttattgacg 60

tattgcttga tcagatattc attttgattt aggtactaaa atg cga ttt tcg ctc   115
                                              Met Arg Phe Ser Leu
                                                1               5

tgc gga ttt cct cta gtt ttt tct ttt aca ttg ctc tca gtc ttc gac   163
Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu Leu Ser Val Phe Asp
                10                  15                  20

act tct ttg agt gct act acg att tct tta acc cca gaa gat agt ttt   211
Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr Pro Glu Asp Ser Phe
            25                  30                  35

cat gga gat agt cag aat gca gaa cgt tct tat aat gtt caa gct ggg   259
His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr Asn Val Gln Ala Gly
        40                  45                  50

gat gtc tat agc ctt act ggt gat gtc tca ata tct aac gtc gat aac   307
Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile Ser Asn Val Asp Asn
    55                  60                  65

tct gca tta aat aaa gcc tgc ttc aat gtg acc tca gga agt gtg acg   355
Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr Ser Gly Ser Val Thr
70                  75                  80                  85

ttc gca gga aat cat cat ggg tta tat ttt aat aat att tcc tca gga   403
Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn Asn Ile Ser Ser Gly
                90                  95                 100

act aca aag gaa ggg gct gta ctt tgt tgc caa gat cct caa gca acg   451
Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln Asp Pro Gln Ala Thr
            105                 110                 115

gca cgt ttt tct ggg ttc tcc acg ctc tct ttt att cag agc ccc gga   499
Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe Ile Gln Ser Pro Gly
        120                 125                 130
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gat att aaa gaa cag gga tgt ctc tat tca aaa aat gca ctt atg ctc   547
Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys Asn Ala Leu Met Leu
    135                 140                 145

tta aac aat tat gta gtg cgt ttt gaa caa aac caa agt aag act aaa   595
Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn Gln Ser Lys Thr Lys
150                 155                 160                 165

ggc gga gct att agt ggg gcg aat gtt act ata gta ggc aac tac gat   643
Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile Val Gly Asn Tyr Asp
                170                 175                 180

tcc gtc tct ttc tat cag aat gca gcc act ttt gga ggt gct atc cat   691
Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe Gly Gly Ala Ile His
            185                 190                 195

tct tca ggt ccc cta cag att gca gta aat cag gca gag ata aga ttt   739
Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln Ala Glu Ile Arg Phe
        200                 205                 210

gca caa aat act gcc aag aat ggt tct gga ggg gct ttg tac tcc gat   787
Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly Ala Leu Tyr Ser Asp
    215                 220                 225

ggt gat att gat att gat cag aat gct tat gtt cta ttt cga gaa aat   835
Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val Leu Phe Arg Glu Asn
230                 235                 240                 245

gag gca ttg act act gct ata ggt aag gga ggg gct gtc tgt tgt ctt   883
Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly Ala Val Cys Cys Leu
                250                 255                 260

ccc act tca gga agt agt act cca gtt cct att gtg act ttc tct gac   931
Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile Val Thr Phe Ser Asp
            265                 270                 275

aat aaa cag tta gtc ttt gaa aga aac cat tcc ata atg ggt ggc gga   979
Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser Ile Met Gly Gly Gly
        280                 285                 290

gcc att tat gct agg aaa ctt agc atc tct tca gga ggt cct act cta  1027
Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser Gly Gly Pro Thr Leu
    295                 300                 305

ttt atc aat aat ata tca tat gca aat tcg caa aat tta ggt gga gct  1075
Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln Asn Leu Gly Gly Ala
310                 315                 320                 325

att gcc att gat act gga ggg gag atc agt tta tca gca gag aaa gga  1123
Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu Ser Ala Glu Lys Gly
                330                 335                 340

aca att aca ttc caa gga aac cgg acg agc tta ccg ttt ttg aat ggc  1171
Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu Pro Phe Leu Asn Gly
            345                 350                 355
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atc cat ctt tta caa aat gct aaa ttc ctg aaa tta cag gcg aga aat   1219
Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys Leu Gln Ala Arg Asn
        360                 365                 370

gga tac tct ata gaa ttt tat gat cct att act tct gaa gca gat ggg   1267
Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr Ser Glu Ala Asp Gly
    375                 380                 385

tct acc caa ttg aat atc aac gga gat cct aaa aat aaa gag tac aca   1315
Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys Asn Lys Glu Tyr Thr
390                 395                 400                 405


ggg acc ata ctc ttt tct gga gaa aag agt cta gca aac gat cct agg   1363
Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu Ala Asn Asp Pro Arg
                410                 415                 420

gat ttt aaa tct aca atc cct cag aac gtc aac ctg tct gca gga tac   1411
Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn Leu Ser Ala Gly Tyr
            425                 430                 435

tta gtt att aaa gag ggg gcc gaa gtc aca gtt tca aaa ttc acg cag   1459
Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val Ser Lys Phe Thr Gln
        440                 445                 450

tct cca gga tcg cat tta gtt tta gat tta gga acc aaa ctg ata gcc   1507
Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly Thr Lys Leu Ile Ala
    455                 460                 465

tct aag gaa gac att gcc atc aca ggc ctc gcg ata gat ata gat agc   1555
Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala Ile Asp Ile Asp Ser
470                 475                 480                 485

tta agc tca tcc tca aca gca gct gtt att aaa gca aac acc gca aat   1603
Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys Ala Asn Thr Ala Asn
                490                 495                 500

aaa cag ata tcc gtg acg gac tct ata gaa ctt atc tcg cct act ggc   1651
Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu Ile Ser Pro Thr Gly
            505                 510                 515

aat gcc tat gaa gat ctc aga atg aga aat tca cag acg ttc cct ctg   1699
Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser Gln Thr Phe Pro Leu
        520                 525                 530

ctc tct tta gag cct gga gcc ggg ggt agt gtg act gta act gct gga   1747
Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val Thr Val Thr Ala Gly
    535                 540                 545

gat ttc cta ccg gta agt ccc cat tat ggt ttt caa ggc aat tgg aaa   1795
Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe Gln Gly Asn Trp Lys
550                 555                 560                 565
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tta gct tgg aca gga act gga aac aaa gtt gga gaa ttc ttc tgg gat    1843
Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly Glu Phe Phe Trp Asp
                570                 575                 580

aaa ata aat tat aag cct aga cct gaa aaa gaa gga aat tta gtt cct    1891
Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu Gly Asn Leu Val Pro
            585                 590                 595

aat atc ttg tgg ggg aat gct gta gat gtc aga tcc tta atg cag gtt    1939
Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg Ser Leu Met Gln Val
        600                 605                 610

caa gag acc cat gca tcg agc tta cag aca gat cga ggg ctg tgg atc    1987
Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp Arg Gly Leu Trp Ile
    615                 620                 625

gat gga att ggg aat ttc ttc cat gta tct gcc tcc gaa gac aat ata    2035
Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala Ser Glu Asp Asn Ile
630                 635                 640                 645

agg tac cgt cat aac agc ggt gga tat gtt cta tct gta aat aat gag    2083
Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu Ser Val Asn Asn Glu
                650                 655                 660

atc aca cct aag cac tat act tcg atg gca ttt tcc caa ctc ttt agt    2131
Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe Ser Gln Leu Phe Ser
            665                 670                 675

aga gac aag gac tat gcg gtt tcc aac aac gaa tac aga atg tat tta    2179
Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu Tyr Arg Met Tyr Leu
        680                 685                 690

gga tcg tat ctc tat caa tat aca acc tcc cta ggg aat att ttc cgt    2227
Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu Gly Asn Ile Phe Arg
    695                 700                 705

tat gct tcg cgt aac cct aat gta aac gtc ggg att ctc tca aga agg    2275
Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly Ile Leu Ser Arg Arg
710                 715                 720                 725

ttt ctt caa aat cct ctt atg att ttt cat ttt ttg tgt gct tat ggt    2323
Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe Leu Cys Ala Tyr Gly
                730                 735                 740

cat gcc acc aat gat atg aaa aca gac tac gca aat ttc cct atg gtg    2371
His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala Asn Phe Pro Met Val
            745                 750                 755

aaa aac agc tgg aga aac aat tgt tgg gct ata gag tgc gga ggg agc    2419
Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile Glu Cys Gly Gly Ser
        760                 765                 770

atg cct cta ttg gta ttt gag aac gga aga ctt ttc caa ggt gcc atc    2467
Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu Phe Gln Gly Ala Ile
    775                 780                 785
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cca ttt atg aaa cta caa tta gtt tat gct tat cat gga gat ttc aaa   2515
Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr His Gly Asp Phe Lys
790                 795                 800                 805

gag acg act gca gat ggc cgt aga ttt agt aat ggg agt tta aca tcg   2563
Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn Gly Ser Leu Thr Ser
                810                 815                 820

att tct gta cct cta ggc ata cgc ttt gag aag ctg gca ctt tct cag   2611
Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys Leu Ala Leu Ser Gln
            825                 830                 835

gat gta ctc tat gac ttt agt ttc tcc tat att cct gat att ttc cgt   2659
Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile Pro Asp Ile Phe Arg
        840                 845                 850

aag gat ccc tca tgt gaa gct gct ctg gtg att agc gga gac tcc tgg   2707
Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile Ser Gly Asp Ser Trp
    855                 860                 865

ctt gtt ccg gca gca cac gta tca aga cat gct ttt gta ggg agt gga   2755
Leu Val Pro Ala Ala His Val Ser Arg His Ala Phe Val Gly Ser Gly
870                 875                 880                 885

acg ggt cgg tat cac ttt aac gac tat act gag ctc tta tgt cga gga   2803
Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu Leu Leu Cys Arg Gly
                890                 895                 900

agt ata gaa tgc cgc ccc cat gct agg aat tat aat ata aac tgt gga   2851
Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr Asn Ile Asn Cys Gly
            905                 910                 915

agc aaa ttt cgt ttt tagaaggttt ccattgcctg tgtggttccg gatcttaact   2906
Ser Lys Phe Arg Phe
        920

ataaatcctg gactatggat cataggcatt gggtttctcg aact                 2950


<210> 7
<211> 1328
<212> DNA
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<220>
<221> CDS
<222> (101)..(1225)

<400> 7
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agcaaccaag caaagaaagg tggtggggtt tatcttgaag atg ccc tca tcc tgg   115
                                              Met Pro Ser Ser Trp
                                                1               5
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aaa agg tta tta cag gtt ctg tct cac aaa ata gca gct aca gaa agt   163
Lys Arg Leu Leu Gln Val Leu Ser His Lys Ile Ala Ala Thr Glu Ser
                 10                  15                  20

ggt ggg ggt atc tac gct aag gat att caa cta caa gct cta cct gga   211
Gly Gly Gly Ile Tyr Ala Lys Asp Ile Gln Leu Gln Ala Leu Pro Gly
             25                  30                  35

agc ttc aca att acc gat aat aaa gtc gaa act agt ctt act act agc   259
Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr Ser Leu Thr Thr Ser
         40                  45                  50

act aat tta tat ggt ggg ggc atc tat tcc agt gga gct gtc acg cta   307
Thr Asn Leu Tyr Gly Gly Gly Ile Tyr Ser Ser Gly Ala Val Thr Leu
     55                  60                  65

acc aat ata tct gga acc ttt ggc att aca gga aac tct gtt atc aat   355
Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly Asn Ser Val Ile Asn
 70                  75                  80                  85

aca gcg aca tcc cag gat gca gat ata caa ggt ggg ggc att tat gca   403
Thr Ala Thr Ser Gln Asp Ala Asp Ile Gln Gly Gly Gly Ile Tyr Ala
                 90                  95                 100

acc acg tct ctc tca ata aat caa tgt aat aca ccc att cta ttt agc   451
Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr Pro Ile Leu Phe Ser
             105                 110                 115

aac aac tct gct gcc act aaa aaa aca tca aca aca aag caa att gct   499
Asn Asn Ser Ala Ala Thr Lys Lys Thr Ser Thr Thr Lys Gln Ile Ala
         120                 125                 130

ggt ggg gct atc ttc tcc gct gca gta act atc gag aat aac tct cag   547
Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile Glu Asn Asn Ser Gln
     135                 140                 145

ccc att att ttc tta aat aat tcc gca aag tcg gaa gca act aca gca   595
Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser Glu Ala Thr Thr Ala
150                 155                 160                 165

gca act gca gga aat aaa gat agc tgt gga gga gcc att gca gct aac   643
Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly Ala Ile Ala Ala Asn
                170                 175                 180

tct gtt act tta aca aat aac cct gaa ata acc ttt aaa gga aat tat   691
Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr Phe Lys Gly Asn Tyr
             185                 190                 195

gca gaa act gga gga gcg att ggc tgt att gat ctt act aat ggc tca   739
Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp Leu Thr Asn Gly Ser
         200                 205                 210

cct ccc cgt aaa gtc tct att gca gac aac ggt tct gtc ctt ttt caa   787
Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly Ser Val Leu Phe Gln
     215                 220                 225
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gac aac tct gcg tta aat cgc gga ggc gct atc tat gga gag act atc   835
Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile Tyr Gly Glu Thr Ile
230                 235                 240                 245

gat atc tcc agg aca ggt gcg act ttc atc ggt aac tct tca aaa cat   883
Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly Asn Ser Ser Lys His
                250                 255                 260

gat gga agt gca att tgc tgt tca aca gcc cta act ctt gcg cca aac   931
Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu Thr Leu Ala Pro Asn
            265                 270                 275

tcc caa ctt atc ttt gaa aac aat aag gtt acg gaa acc aca gcc act   979
Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr Glu Thr Thr Ala Thr
        280                 285                 290

aca aaa gct tcc ata aat aat tta gga gct gca att tat gga aat aat   1027
Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala Ile Tyr Gly Asn Asn
    295                 300                 305

gag act agt gac gtc act atc tct tta tca gct gag aat gga agt att   1075
Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala Glu Asn Gly Ser Ile
310                 315                 320                 325

ttc ttt aaa aac aat cta tgc aca gca aca aac aaa tac tgc agt att   1123
Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn Lys Tyr Cys Ser Ile
                330                 335                 340

gct gga aac gta aaa ttt aca gca ata gaa gct tca gca ggg aaa gct   1171
Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala Ser Ala Gly Lys Ala
            345                 350                 355

ata tct ttc tat gat gca gtt aac gtt cca cca aag aaa caa ttg ctc   1219
Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro Lys Lys Gln Leu Leu
        360                 365                 370

aag agc taaattaaat gaaaaagcga caagtacang gacgtttcta ntttctgggg   1275
Lys Ser
    375

gacttcacgg aaataaatcc ctattccaca gaaagtcact tcgccctngg gat       1328


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atgggagtat ttttgataaa aagcttttcc ccaaagacac atg aaa tat tct tta   115
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                                                    Met Lys Tyr Ser Leu
                                                      1               5

cct tgg cta ctt acc tct tcg gct tta gtt ttc tcc cta cat cca cta   163
Pro Trp Leu Leu Thr Ser Ser Ala Leu Val Phe Ser Leu His Pro Leu
                  10                  15                  20

atg gct gct aac acg gat ctc tca tca tcc gat aac tat gaa aat ggt   211
Met Ala Ala Asn Thr Asp Leu Ser Ser Ser Asp Asn Tyr Glu Asn Gly
              25                  30                  35

agt agt ggt agc gca gca ttc act gcc aag gaa act tcg gat gct tca   259
Ser Ser Gly Ser Ala Ala Phe Thr Ala Lys Glu Thr Ser Asp Ala Ser
          40                  45                  50

gga act acc tac act ctc act agc gat gtt tct att acg aat gta tct   307
Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser Ile Thr Asn Val Ser
      55                  60                  65

gca att act cct gca gat aaa agc tgt ttt aca aac aca gga gga gca   355
Ala Ile Thr Pro Ala Asp Lys Ser Cys Phe Thr Asn Thr Gly Gly Ala
  70                  75                  80                  85

ttg agt ttt gtt gga gct gat cac tca ttg gtt ctg caa acc ata gcg   403
Leu Ser Phe Val Gly Ala Asp His Ser Leu Val Leu Gln Thr Ile Ala
                  90                  95                 100

ctt acg cat gat ggt gct gca att aac aat acc aac aca gct ctt tct   451
Leu Thr His Asp Gly Ala Ala Ile Asn Asn Thr Asn Thr Ala Leu Ser
              105                 110                 115

ttc tca gga ttc tcg tca ctc tta atc gac tca gct cca gca aca gga   499
Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser Ala Pro Ala Thr Gly
          120                 125                 130

act tcg ggc ggc aag ggt gct att tgt gtg aca aat aca gag gga ggt   547
Thr Ser Gly Gly Lys Gly Ala Ile Cys Val Thr Asn Thr Glu Gly Gly
      135                 140                 145

act gcg act ttt act gac aat gcc agt gtc acc ctc caa aaa aat act   595
Thr Ala Thr Phe Thr Asp Asn Ala Ser Val Thr Leu Gln Lys Asn Thr
150                 155                 160                 165

tca gaa aaa gat gga gct gca gtt tct gcc tac agc atc gat ctt gct   643
Ser Glu Lys Asp Gly Ala Ala Val Ser Ala Tyr Ser Ile Asp Leu Ala
                  170                 175                 180

aag act acg aca gca gct ctc tta gat caa aat act agc aca aaa aat   691
Lys Thr Thr Thr Ala Ala Leu Leu Asp Gln Asn Thr Ser Thr Lys Asn
              185                 190                 195

ggc ggg gcc ctc tgt agt aca gca aac act aca gtc caa gga aac tca   739
Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr Val Gln Gly Asn Ser
          200                 205                 210
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gga acg gtg acc ttc tcc tca aat act gct aca gat aaa ggt ggg ggg   787
Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr Asp Lys Gly Gly Gly
    215                 220                 225

atc tac tca aaa gaa aag gat agc acg cta gat gcc aat aca gga gtc   835
Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp Ala Asn Thr Gly Val
230                 235                 240                 245

gtt acc ttc aaa tct aat act gca aag acg ggg ggt gct tgg agc tct   883
Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly Gly Ala Trp Ser Ser
                250                 255                 260

gat gac aat ctt gct ctt acc ggc aac act caa gta ctt ttt cag gaa   931
Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln Val Leu Phe Gln Glu
            265                 270                 275

aat aaa aca acc ggc tca gca gca cag gca aat aac ccg gaa ggt tgt   979
Asn Lys Thr Thr Gly Ser Ala Ala Gln Ala Asn Asn Pro Glu Gly Cys
        280                 285                 290

ggt ggg gca atc tgt tgt tat ctt gct aca gca aca gac aaa act gga   1027
Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala Thr Asp Lys Thr Gly
    295                 300                 305

tta gcc att tct cag aat caa gaa atg agc ttc act agt aat aca aca   1075
Leu Ala Ile Ser Gln Asn Gln Glu Met Ser Phe Thr Ser Asn Thr Thr
310                 315                 320                 325

act gcg aat ggt gga gcg atc tac gct act aaa tgt act ctg gat gga   1123
Thr Ala Asn Gly Gly Ala Ile Tyr Ala Thr Lys Cys Thr Leu Asp Gly
                330                 335                 340

aac aca act ctt acc ttc gat cag aat act gcg aca gca gga tgt ggc   1171
Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala Thr Ala Gly Cys Gly
            345                 350                 355

gga gct atc tat aca gaa act gaa gat ttt tct ctt aag gga agt acg   1219
Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser Leu Lys Gly Ser Thr
        360                 365                 370

gga acc gtg acc ttc agc aca aat aca gca aag aca ggc ggc gcc tta   1267
Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys Thr Gly Gly Ala Leu
    375                 380                 385

tat tct aaa gga aac agc tcg ctg act gga aat acc aac ctg ctc ttt   1315
Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn Thr Asn Leu Leu Phe
390                 395                 400                 405

tca ggg aac aaa gct acg ggc ccg agt aat tct tca gca aat caa gag   1363
Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser Ser Ala Asn Gln Glu
                410                 415                 420

ggt tgc ggt ggg gca atc cta gcc ttt att gat tca gga tcc gta agc   1411
Gly Cys Gly Gly Ala Ile Leu Ala Phe Ile Asp Ser Gly Ser Val Ser
            425                 430                 435
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gat aaa aca gga cta tcg att gca aac aac caa gaa gtc agc ctc act   1459
Asp Lys Thr Gly Leu Ser Ile Ala Asn Asn Gln Glu Val Ser Leu Thr
        440                 445                 450

agt aat gct gca aca gta agt ggt ggt gcg atc tat gct acc aaa tgt   1507
Ser Asn Ala Ala Thr Val Ser Gly Gly Ala Ile Tyr Ala Thr Lys Cys
    455                 460                 465

act cta act gga aac ggc tcc ctg acc ttt gac ggc aat act gct gga   1555
Thr Leu Thr Gly Asn Gly Ser Leu Thr Phe Asp Gly Asn Thr Ala Gly
470                 475                 480                 485

act tca gga ggg gcg atc tat aca gaa act gaa gat ttt act ctt aca   1603
Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Thr Leu Thr
                490                 495                 500

gga agt aca gga acc gtg acc ttc agc aca aat aca gca aag aca ggc   1651
Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys Thr Gly
            505                 510                 515

ggc gcc tta tat tct aaa ggc aac aac tct ctg tct ggt aat acc aac   1699
Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu Ser Gly Asn Thr Asn
        520                 525                 530

ctg ctc ttt tca ggg aac aaa gct acg ggc ccg agt aat tct tca gca   1747
Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser Ser Ala
    535                 540                 545

aat caa gag ggt tgc ggt ggg gca atc cta tcg ttt ctt gag tca gca   1795
Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser Phe Leu Glu Ser Ala
550                 555                 560                 565

tct gta agt act aaa aaa gga ctc tgg att gaa gat aac gaa aac gtg   1843
Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu Asp Asn Glu Asn Val
                570                 575                 580

agt ctc tct ggt aat act gca aca gta agt ggc ggt gcg atc tat gcg   1891
Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly Gly Ala Ile Tyr Ala
            585                 590                 595

acc aag tgt gct ctg cat gga aac acg act ctt acc ttt gat ggc aat   1939
Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu Thr Phe Asp Gly Asn
        600                 605                 610

act gcc gaa act gca gga gga gcg atc tat aca gaa acc gaa gat ttt   1987
Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe
    615                 620                 625

act ctt acg gga agt acg gga acc gtg acc ttc agc aca aat aca gca   2035
Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala
630                 635                 640                 645

aag aca gca ggg gct cta cat act aaa gga aat act tcc ttt acc aaa   2083
Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn Thr Ser Phe Thr Lys
                650                 655                 660
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aat aag gct ctt gta ttt tct gga aat tca gca aca gca aca gca aca   2131
Asn Lys Ala Leu Val Phe Ser Gly Asn Ser Ala Thr Ala Thr Ala Thr
            665                 670                 675

aca act aca gat caa gaa ggt tgt ggt gga gcg atc ctc tgt aat atc   2179
Thr Thr Thr Asp Gln Glu Gly Cys Gly Gly Ala Ile Leu Cys Asn Ile
        680                 685                 690

tca gag tct gac ata gct aca aaa agc tta act ctt act gaa aat gag   2227
Ser Glu Ser Asp Ile Ala Thr Lys Ser Leu Thr Leu Thr Glu Asn Glu
    695                 700                 705

agt tta agt ttc att aac aat acg gca aaa aga agt ggt ggt ggt att   2275
Ser Leu Ser Phe Ile Asn Asn Thr Ala Lys Arg Ser Gly Gly Gly Ile
710                 715                 720                 725

tat gct cct aag tgt gta atc tca ggc agt gaa tcc ata aac ttt gat   2323
Tyr Ala Pro Lys Cys Val Ile Ser Gly Ser Glu Ser Ile Asn Phe Asp
                730                 735                 740

ggc aat act gct gaa act tcg gga gga gcg att tat tcg aaa aac ctt   2371
Gly Asn Thr Ala Glu Thr Ser Gly Gly Ala Ile Tyr Ser Lys Asn Leu
            745                 750                 755

tcg att aca gct aac ggt cct gtc tcc ttt acc aat aat tct gga ggc   2419
Ser Ile Thr Ala Asn Gly Pro Val Ser Phe Thr Asn Asn Ser Gly Gly
        760                 765                 770

aag gga ggc gcc att tat ata gcc gat agc gga gaa ctt tcc tta gag   2467
Lys Gly Gly Ala Ile Tyr Ile Ala Asp Ser Gly Glu Leu Ser Leu Glu
    775                 780                 785

gct att gat ggg gat att act ttc tca ggg aac cga gcg act gag gga   2515
Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn Arg Ala Thr Glu Gly
790                 795                 800                 805

act tca act ccc aac tcg atc cat tta ggt gcc agg ggc aag atc act   2563
Thr Ser Thr Pro Asn Ser Ile His Leu Gly Ala Arg Gly Lys Ile Thr
                810                 815                 820

aag ctt gca gca gct cct ggt cat acg att tat ttt tat gat cct att   2611
Lys Leu Ala Ala Ala Pro Gly His Thr Ile Tyr Phe Tyr Asp Pro Ile
            825                 830                 835

acg atg gaa gct cct gca tct gga gga aca ata gag gag tta gtc atc   2659
Thr Met Glu Ala Pro Ala Ser Gly Gly Thr Ile Glu Glu Leu Val Ile
        840                 845                 850

aat cct gtt gtc aaa gct att gtt cct cct ccc caa cca aaa aat ggt   2707
Asn Pro Val Val Lys Ala Ile Val Pro Pro Pro Gln Pro Lys Asn Gly
    855                 860                 865

cct ata tagaagaaaa acgaatgctc tttgtaaggc tcaagagtaa aaaattctaa   2763
Pro Ile
870
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aggtattctc tcaataggtt ctgaagtgct gccgtagaat tcataaatat ctc        2816


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taaatttata aacttctaga caacaaattg atgatttttt atg aca aac tct att   115
                                              Met Thr Asn Ser Ile
                                                1               5

ttc ata tca aag ttt gga tgt tta tgc gac cca ttt gtc tca gca ttt   163
Phe Ile Ser Lys Phe Gly Cys Leu Cys Asp Pro Phe Val Ser Ala Phe
                10                  15                  20

tat ccc act gcg cta tgt tgt tcc tta tca gga aat gaa gtc cct aac   211
Tyr Pro Thr Ala Leu Cys Cys Ser Leu Ser Gly Asn Glu Val Pro Asn
            25                  30                  35

ctc gcc tct tgt cag atg tct aga aaa gac atc tct gct ttc cac acg   259
Leu Ala Ser Cys Gln Met Ser Arg Lys Asp Ile Ser Ala Phe His Thr
        40                  45                  50

tct cca agc ttc cgt ctg aat gta act cca gag ccc ttg gtt tcc tcc   307
Ser Pro Ser Phe Arg Leu Asn Val Thr Pro Glu Pro Leu Val Ser Ser
    55                  60                  65

ttt cgt ccc tct aat ctt ctt aat gga ttc ggt cac gat ata acc cag   355
Phe Arg Pro Ser Asn Leu Leu Asn Gly Phe Gly His Asp Ile Thr Gln
70                  75                  80                  85

gac atc aca att aca gga aac tct atc aat tct gtt ata gat tat aac   403
Asp Ile Thr Ile Thr Gly Asn Ser Ile Asn Ser Val Ile Asp Tyr Asn
                90                  95                  100

tac cac tac gag gat gga ggc att ctt gca tgt aaa aat ttg ttc att   451
Tyr His Tyr Glu Asp Gly Gly Ile Leu Ala Cys Lys Asn Leu Phe Ile
            105                 110                 115

tct gaa aat aaa gga aac tta agt ttt gaa agg aat agc tcc cac agt   499
Ser Glu Asn Lys Gly Asn Leu Ser Phe Glu Arg Asn Ser Ser His Ser
        120                 125                 130

tct gga ggg gct ctc tac agt gtt cgg gaa tgc tgg att tct aag aat   547
Ser Gly Gly Ala Leu Tyr Ser Val Arg Glu Cys Trp Ile Ser Lys Asn
    135                 140                 145
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cag aac tac tcg ttt att tca aat gcg gct tcc tta gct act act aca   595
Gln Asn Tyr Ser Phe Ile Ser Asn Ala Ala Ser Leu Ala Thr Thr Thr
150                 155                 160                 165

act tca gga ttt ggt ggg gct ata cat gca cta gat agc tat att aca   643
Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu Asp Ser Tyr Ile Thr
                170                 175                 180

aat aac tta gga gaa gga caa ttc tta gat aat gtc tct aaa aat aga   691
Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn Val Ser Lys Asn Arg
            185                 190                 195

gga gga gct atc tat gtt ggg gtg agt tta tca atc aca gac aac tta   739
Gly Gly Ala Ile Tyr Val Gly Val Ser Leu Ser Ile Thr Asp Asn Leu
        200                 205                 210

ggt cct atc gtt atc aag aaa aat caa aca tta gaa gat tcc agc ttt   787
Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu Glu Asp Ser Ser Phe
    215                 220                 225

gga gga ggc atc ttc tgc aga gcc gta aat ata gaa agg aat tat caa   835
Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile Glu Arg Asn Tyr Gln
230                 235                 240                 245

aac atc caa atc aat gat aat gct tca gga caa ggg gtg gta tat ttt   883
Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln Gly Val Val Tyr Phe
                250                 255                 260

ctg ccc cta gga gtc att atc tct tca aat aaa gaa att ata gag atc   931
Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys Glu Ile Ile Glu Ile
            265                 270                 275

agc aat cac tcc gca tcc tca att aac aca gca tca gga aaa cta tat   979
Ser Asn His Ser Ala Ser Ser Ile Asn Thr Ala Ser Gly Lys Leu Tyr
        280                 285                 290

ccc ggt ggt ggc ggt atc atg tgt acc tcc ctt agt cat gag aac aat  1027
Pro Gly Gly Gly Gly Ile Met Cys Thr Ser Leu Ser His Glu Asn Asn
    295                 300                 305


ccc aaa ggt ctt atc ttt aac aat aaa acg gca gca ctt agc ggc gga  1075
Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala Ala Leu Ser Gly Gly
310                 315                 320                 325

gta tac aca cga gat ctt tca tct tcc aaa ata acg gtc cgc aca gca  1123
Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile Thr Val Arg Thr Ala
                330                 335                 340

ttt att aat aac tct gcg act tca gga ggg gct ctc atc aat ctt tct  1171
Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala Leu Ile Asn Leu Ser
            345                 350                 355

ggt ata gga agt act cct caa aat ttc ttc ctc tct gca gac tac ggc  1219
Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu Ser Ala Asp Tyr Gly
        360                 365                 370
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gat att cta ttt aac aat aat aca atc aca tct tct tct cct caa ccc   1267
Asp Ile Leu Phe Asn Asn Asn Thr Ile Thr Ser Ser Ser Pro Gln Pro
    375                 380                 385

gga tat aga aat gca ctc tat gct gct ccg ggg att aac tta aaa cta   1315
Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly Ile Asn Leu Lys Leu
390                 395                 400                 405

gga gca aga cag ggt tat aaa att ctc ttt tat gat cct ata gat cac   1363
Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr Asp Pro Ile Asp His
                410                 415                 420

gat cag acg aca aca gat cct ata gta ttt aat tat gaa ccc cat cac   1411
Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn Tyr Glu Pro His His
            425                 430                 435

ctt ggc acc gtg ttg ttt tcc gga atc aat gta gat tct aac gca aca   1459
Leu Gly Thr Val Leu Phe Ser Gly Ile Asn Val Asp Ser Asn Ala Thr
        440                 445                 450

aat cca ttg aac ttc cta tca aaa ttt tct aac tct tca cga ctt gaa   1507
Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn Ser Ser Arg Leu Glu
    455                 460                 465

agg ggt gtg ctc gct att gaa gat cgg gct gct att tct tgc aaa acc   1555
Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala Ile Ser Cys Lys Thr
470                 475                 480                 485

cta tcg caa act ggg ggc att cta cgt tta gga aac gca gca tta atc   1603
Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly Asn Ala Ala Leu Ile
                490                 495                 500

agg acg aaa ggc ccg gga agc tcc ata aat ttt aat gca atc gcg atc   1651
Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe Asn Ala Ile Ala Ile
            505                 510                 515

aat ctt cct tct att tta caa tca gaa gcc tca gct cca aag ttc tgg   1699
Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser Ala Pro Lys Phe Trp
        520                 525                 530

att tat cct aca tta aca gga tcc acc tat tct gaa gac act tct tct   1747
Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser Glu Asp Thr Ser Ser
    535                 540                 545

act atc act ctc tca gga ccc ttg act ttt cta aac gat gaa aat gaa   1795
Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu Asn Asp Glu Asn Glu
550                 555                 560                 565

aac ccc tat gat agc tta gat ctc tct gaa cct cga aag gat atc ccc   1843
Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro Arg Lys Asp Ile Pro
                570                 575                 580

cct cct cta cct cct cga tgt gac tgc aaa aaa atc gat act tcg aat   1891
Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys Ile Asp Thr Ser Asn
            585                 590                 595
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ctc att gta gaa gcc atg aac tta gat gag cac tat gga tat cag gga   1939
Leu Ile Val Glu Ala Met Asn Leu Asp Glu His Tyr Gly Tyr Gln Gly
        600                 605                 610

atc tgg tct ccc tat tgg atg gaa act acg act aca aca agc tct aca   1987
Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr Thr Thr Ser Ser Thr
    615                 620                 625

gta ccg gaa cag acc aat aca aac cac agg cag ctc tac gta gac tgg   2035
Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln Leu Tyr Val Asp Trp
630                 635                 640                 645

act cct gta gga tac cgc cct aac ccg gaa cgt cac gga gaa ttt att   2083
Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg His Gly Glu Phe Ile
                650                 655                 660

gct aat acc tta tgg cag tct gcc tat aac gct ctg tta gga atc cgc   2131
Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala Leu Leu Gly Ile Arg
            665                 670                 675

atc tta cct cca caa aac ctc aaa gag cat gac ctt gaa gcc tct ctg   2179
Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp Leu Glu Ala Ser Leu
        680                 685                 690

caa gga ctc ggg ctt cta att aac caa cat aat cgc gag gga cgc aaa   2227
Gln Gly Leu Gly Leu Leu Ile Asn Gln His Asn Arg Glu Gly Arg Lys
    695                 700                 705

ggc ttc cga aac cat act acg ggc tat gca gca aca acc tca gca aaa   2275
Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala Thr Thr Ser Ala Lys
710                 715                 720                 725

act gca gca cga cat agt ttc tct tta gga ttc gca caa atg ttc tcc   2323
Thr Ala Ala Arg His Ser Phe Ser Leu Gly Phe Ala Gln Met Phe Ser
                730                 735                 740

aaa act aga gaa cgt caa tct cca agt acg act tcc tcc cac aac tac   2371
Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr Ser Ser His Asn Tyr
            745                 750                 755

ttt gca gga ctc cgc ttc gac agt ctc ctc ttc agg gac ttc atc tct   2419
Phe Ala Gly Leu Arg Phe Asp Ser Leu Leu Phe Arg Asp Phe Ile Ser
        760                 765                 770

aca ggg cta tcc cta ggt tat agc tac gga gat cac cat atg ctt tgc   2467
Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp His His Met Leu Cys
    775                 780                 785

cac tat aca gaa atc tta aaa ggg tcg tcc aaa gcc ttc ttt aat aac   2515
His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys Ala Phe Phe Asn Asn
790                 795                 800                 805

cac act ttg gta gcc tct cta gac tgc aca ttc tta cca gct aga atc   2563
His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe Leu Pro Ala Arg Ile
                810                 815                 820
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acc cgc act ctc gaa ctc cag ccc ttt atc agt gcc att gct ctg cgc   2611
Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser Ala Ile Ala Leu Arg
            825                 830                 835

tgt tcc cag gcc tcg ttc caa gaa act gga gac cat ata aga aaa ttc   2659
Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp His Ile Arg Lys Phe
        840                 845                 850

cat cca aaa cat ccc ctt aca gat ctt tcc tct ccc ata ggc ttc cgt   2707
His Pro Lys His Pro Leu Thr Asp Leu Ser Ser Pro Ile Gly Phe Arg
    855                 860                 865

tct gaa tgg aaa act tca cat cat atc ccc atg cta tgg act acg gaa   2755
Ser Glu Trp Lys Thr Ser His His Ile Pro Met Leu Trp Thr Thr Glu
870                 875                 880                 885

ata tcc tac gta cct acc cta tac aga aaa aat cca gaa atg ttc acg   2803
Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn Pro Glu Met Phe Thr
                890                 895                 900

aca cta ctc atc agc aat gga aca tgg aca aca caa gca act ccc gtc   2851
Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr Gln Ala Thr Pro Val
            905                 910                 915

tcc tat aat tcc gta gct gca aaa ata aaa aat act tcc caa ctt ttc   2899
Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn Thr Ser Gln Leu Phe
        920                 925                 930

tca aga gta acc tta tcc tta gat tat tca gct caa gtc tcc tcg tca   2947
Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala Gln Val Ser Ser Ser
    935                 940                 945

act gta ggt caa tac ctt aaa gct gag agt cat tgc aca ttt           2989
Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His Cys Thr Phe
950                 955                 960

taaccacaaa gaaaacatca aggaataaac agtgcaaaat aacagatccc ttagtaaatc 3049

ttccttcttt gttggagcct taattttagg taaaactaca ata                   3092
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<222> (101)..(1642)

<400> 10
aaacagttaa ataattaata gacaataatc tattcttatt gacttctttt tttcttgttt 60

attaaagttg cttcaacctt attgatttaa cgaggaaacc atg acc ata ctt cga   115

```
                                                    Met Thr Ile Leu Arg
                                                      1               5

aat ttt ctt acc tgc tcg gct tta ttc ctc gct ctc cct gca gca gca   163
Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala Leu Pro Ala Ala Ala
                    10                  15                  20

caa gtt gta tat ctt cat gaa agt gat ggt tat aac ggt gct atc aat   211
Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr Asn Gly Ala Ile Asn
                25                  30                  35

aat aaa agc tta gaa cct aaa att acc tgt tat cca gaa gga act tct   259
Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr Pro Glu Gly Thr Ser
            40                  45                  50

tac atc ttt cta gat gac gtg agg att tcc aac gtt aag cat gat caa   307
Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn Val Lys His Asp Gln
        55                  60                  65

gaa gat gct ggg gtt ttt ata aat cga tct ggg aat ctt ttt ttc atg   355
Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly Asn Leu Phe Phe Met
    70                  75                  80                  85

ggc aac cgt tgc aac ttc act ttt cac aac ctt atg acc gag ggt ttt   403
Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu Met Thr Glu Gly Phe
                90                  95                  100

ggc gct gcc att tcg aac cgc gtt gga gac acc act ctc act ctc tct   451
Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr Thr Leu Thr Leu Ser
            105                 110                 115

aat ttt tct tac tta gcg ttc acc tca gca cct cta cta cct caa gga   499
Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro Leu Leu Pro Gln Gly
        120                 125                 130

caa gga gcg att tat agt ctt ggt tcc gtg atg atc gaa aat agt gag   547
Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met Ile Glu Asn Ser Glu
    135                 140                 145

gaa gtg act ttc tgt ggg aac tac tct tcg tgg agt gga gct gcg att   595
Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp Ser Gly Ala Ala Ile
150                 155                 160                 165

tat act ccc tac ctt tta ggt tct aag gcg agt cgt cct tca gta aat   643
Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser Arg Pro Ser Val Asn
                170                 175                 180

ctc agc ggg aac cgc tac ctg gtg ttt aga gac aat gtg agc caa gtt   691
Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp Asn Val Ser Gln Val
            185                 190                 195

tat ggc ggc gcc ata tct acc cac aat ctc aca ctc acg act cga gga   739
Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr Leu Thr Thr Arg Gly
        200                 205                 210
```

```
cct tcg tgt ttt gaa aat aat cat gct tat cat gac gtg aat agt aat   787
Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His Asp Val Asn Ser Asn
    215                 220                 225

gga gga gcc att gcc att gct cct gga gga tcg atc tct ata tcc gtg   835
Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser Ile Ser Ile Ser Val
230                 235                 240                 245

aaa agc gga gat ctc atc ttc aaa gga aat aca gca tca caa gac gga   883
Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr Ala Ser Gln Asp Gly
                250                 255                 260

aat aca ata cac aac tcc atc cat ctg caa tct gga gca cag ttt aag   931
Asn Thr Ile His Asn Ser Ile His Leu Gln Ser Gly Ala Gln Phe Lys
            265                 270                 275

aac cta cgt gct gtt tca gaa tcc gga gtt tat ttc tat gat cct ata   979
Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr Phe Tyr Asp Pro Ile
        280                 285                 290

agc cat agc gag tcg cat aaa att aca gat ctt gta atc aat gct cct   1027
Ser His Ser Glu Ser His Lys Ile Thr Asp Leu Val Ile Asn Ala Pro
    295                 300                 305

gaa gga aag gaa act tat gaa gga aca att agc ttc tca gga cta tgc   1075
Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser Phe Ser Gly Leu Cys
310                 315                 320                 325

ctg gat gat cat gaa gtt tgt gcg gaa aat ctt act tcc aca atc cta   1123
Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu Thr Ser Thr Ile Leu
                330                 335                 340

caa gat gtc aca tta gca gga gga act ctc tct cta tcg gat ggg gtt   1171
Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser Leu Ser Asp Gly Val
            345                 350                 355

acc ttg caa ctg cat tct ttt aag cag gaa gca agc tct acg ctt act   1219
Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala Ser Ser Thr Leu Thr
        360                 365                 370

atg tct cca gga acc act ctg ctc tgc tca gga gat gct cgg gtt cag   1267
Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly Asp Ala Arg Val Gln
    375                 380                 385

aat ctg cac atc ctg att gaa gat acc gac aac ttt gtt cct gta agg   1315
Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn Phe Val Pro Val Arg
390                 395                 400                 405

att cgc gcc gag gac aag gat gct ctt gtc tca tta gaa aaa ctt aaa   1363
Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser Leu Glu Lys Leu Lys
                410                 415                 420

gtt gcc ttt gag gct tat tgg tcc gtc tat gac ttt cct caa ttt aag   1411
Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp Phe Pro Gln Phe Lys
            425                 430                 435
```

```
gaa gcc ttt acg att cct ctt ctt gaa ctt cta ggg cct tct ttt gac   1459
Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu Gly Pro Ser Phe Asp
        440                 445                 450

agt ctt ctc cta ggg gag acc act ttg gag aga acc caa gtc aca aca   1507
Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg Thr Gln Val Thr Thr
    455                 460                 465

gag aat gac gcc gtt cga ggt ttc tgg tcc cta agc tgg gaa gag tac   1555
Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu Ser Trp Glu Glu Tyr
470                 475                 480                 485

ccc cct tct ctg gat aaa gac aga agg atc aca cca act aag aaa act   1603
Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr Pro Thr Lys Lys Thr
                490                 495                 500

gtt ttc ctc act tgg aat cct gag atc act tct acg cca taatctctaa    1652
Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser Thr Pro
            505                 510

gtctacacta taattaaggg aatccccttt aagaagattt tgggacctat ctgtattcag 1712

agataggtcc ctctatgcac acatgttcac gag                              1745


<210> 11
<211> 1100
<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (101)..(967)

<400> 11
tttggaacct taatgatctc tggagggtgg cttagcaata tgattttacg ctttgcaggt 60

cagattttcc aaaacttcta taaatggaaa taaagagctt atg gga atc tct cta   115
                                        Met Gly Ile Ser Leu
                                          1               5

cca gag ctt ttt tcc aac cta ggt tct gct tac tta gat tat atc ttt   163
Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr Leu Asp Tyr Ile Phe
                10                  15                  20

caa cat cct ccg gcc tat gtt tgg tca gtt ttt ctt ctt tta tta gcc   211
Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe Leu Leu Leu Leu Ala
            25                  30                  35

cgt ctg ctt cct att ttt gct gta gct ccc ttc tta gga gca aag ctc   259
Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe Leu Gly Ala Lys Leu
        40                  45                  50

ttt ccc tcc cct att aaa atc ggg att agt ctc tct tgg ctt gca atc   307
Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu Ser Trp Leu Ala Ile
    55                  60                  65
```

```
atc ttt cca aaa gtc ttg gcg gat acg cag atc aca aat tac atg gat   355
Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile Thr Asn Tyr Met Asp
 70                  75                  80                  85

aac aat ctc ttt tat gtt tta ctt gtg aag gag atg atc ata ggc att   403
Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu Met Ile Ile Gly Ile
                 90                  95                 100

gtg ata ggc ttt gtt tta gca ttt ccc ttt tat gct gca caa tcg gca   451
Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr Ala Ala Gln Ser Ala
            105                 110                 115

gga tct ttc atc act aac caa caa ggg att cag ggt tta gag ggc gcg   499
Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln Gly Leu Glu Gly Ala
        120                 125                 130

aca tcc ctg att tcc att gag cag acc tct ccg cat ggc att tta tac   547
Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro His Gly Ile Leu Tyr
    135                 140                 145

cat tac ttc gtg act att att ttt tgg tta gtg ggt ggt cac cgt att   595
His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val Gly Gly His Arg Ile
150                 155                 160                 165

gta atc tct ttg tta ttg caa act ctt gaa gtc att ccg atc cat agt   643
Val Ile Ser Leu Leu Leu Gln Thr Leu Glu Val Ile Pro Ile His Ser
                170                 175                 180

ttc ttt cct gcc gag atg atg agc tta agt gcc ccg att tgg att act   691
Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala Pro Ile Trp Ile Thr
            185                 190                 195

atg atc aag atg tgc cag ctc tgt ctc gtg atg acc ata cag ctg agt   739
Met Ile Lys Met Cys Gln Leu Cys Leu Val Met Thr Ile Gln Leu Ser
        200                 205                 210

gct cct gca gct ttg gcg atg tta atg tcc gac cta ttc tta ggg att   787
Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp Leu Phe Leu Gly Ile
    215                 220                 225

att aac cgt atg gca cct caa gtt cag gtc atc tac ctc ctc tct gcc   835
Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile Tyr Leu Leu Ser Ala
230                 235                 240                 245

ctt aag gct ttc atg ggt ctt ctc ttt ctc acc ctg gcg tgg tgg ttc   883
Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr Leu Ala Trp Trp Phe
                250                 255                 260

ata att aag cag ata gat tat ttc act ctt gct tgg ttc aaa gaa gtc   931
Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala Trp Phe Lys Glu Val
            265                 270                 275

ccc att atg ctc cta ggt tcc aac cct caa gta ctc taatccccta        977
Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val Leu
        280                 285
```

```
ggctcttatc gtgactctta tctggagatg cgctcactta cgaatcttag cgcactgttt 1037

atggattatc ttagggaatc tctcgcatat tcttttgtaa tctaagaatc tataaattca 1097

aga                                                                1100
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<210> 12
<211> 950
<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (101)..(895)

<400> 12

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ccagtgataa agactctagt gataaagatg ctccagaagg aagcaatgaa attgagggtg 60

cttagtgact gccaacactt ttggaactct agacatcttg atg aag cac tcc aag   115
                                          Met Lys His Ser Lys
                                            1               5

gaa gat gac ctc tcc agg ttt ctt cct aaa aat ctt ctt gtt gaa tct   163
Glu Asp Asp Leu Ser Arg Phe Leu Pro Lys Asn Leu Leu Val Glu Ser
                10                  15                  20

cct cat ccc gaa gaa atc cct tta aaa tct tta tct ttt acg atg agt   211
Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu Ser Phe Thr Met Ser
            25                  30                  35

tgg cta cct aca att cat cct tca tgg att acc att gcc atg aaa gag   259
Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr Ile Ala Met Lys Glu
        40                  45                  50

ttc cct cct gaa atc caa ggt caa tta tta gcg tgg ttg cca gag cct   307
Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala Trp Leu Pro Glu Pro
    55                  60                  65

tta gtt caa gaa att cta ccc tta ctg cct ggc atc tct ata gcc cca   355
Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly Ile Ser Ile Ala Pro
70                  75                  80                  85

cat cgc tgt gca cct ttc gga gcc ttc tat ctt cta gat atg cta agt   403
His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu Leu Asp Met Leu Ser
                90                  95                  100

aaa aag atc cgt cct tgt gga att aca gaa gaa atc ttt ctt cct gca   451
Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu Ile Phe Leu Pro Ala
            105                 110                 115

tcc tca gca aat gct ata ctt tac tat aca ggt cct gta aag atc gct   499
Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly Pro Val Lys Ile Ala
        120                 125                 130
```

```
tta atc aac tgc cta ggt ctt tat tct att gct aaa gag ttg aag cac   547
Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala Lys Glu Leu Lys His
    135                 140                 145

att ctg gat aag gtt gtg att gaa cga gtg aag aat gct ctc tcc cct   595
Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys Asn Ala Leu Ser Pro
150                 155                 160                 165

aca gag aaa ctc ttt ctt acc tac tgc caa tct cat ccg atg aaa cat   643
Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser His Pro Met Lys His
                170                 175                 180

tta gaa act acg aat ttt ctt tct tct tgg act act gat gca gaa tta   691
Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr Thr Asp Ala Glu Leu
            185                 190                 195

cga cag ttc gtt cat aag caa ggg tta gag ttt tta ggt aaa gca tta   739
Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe Leu Gly Lys Ala Leu
        200                 205                 210

aca aaa gaa aac gct tct ttt cta tgg tat ttt cta cgt agg tta gat   787
Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe Leu Arg Arg Leu Asp
    215                 220                 225

gtc ggt cga gca tat atc gtc gag cag act tta aaa aca tgg tat gac   835
Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu Lys Thr Trp Tyr Asp
230                 235                 240                 245

cat ccc tat gtg gat tat ttt aag tcc cgc cta gaa caa tgc atg aaa   883
His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu Glu Gln Cys Met Lys
                250                 255                 260

gtc tta gtg aaa taaaagcttt ataagtaaag atttagcttt atacaaagta       935
Val Leu Val Lys
            265

tagaaaaata acacg                                                 950
```

<210> 13
<211> 500
<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (101)..(385)

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<400> 13
cgatttcgtt acctttaaag ttacttttga tcgtcatggt agacggatgg acattactgc 60

tccaagggct tatgatcagc tttaaataag gacacgtgcc atg tta gca ttt ttc   115
                                            Met Leu Ala Phe Phe
                                              1               5
```

```
gca act agt ttc aaa tct gtt ctt ttt gag tac tcc tac caa tca tta   163
Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr Ser Tyr Gln Ser Leu
                 10                  15                  20

tta ctt att ttg att gtt tcg gca cct ccc atc atc tta gct tcc ata   211
Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile Ile Leu Ala Ser Ile
             25                  30                  35

gtc ggg att atg gtt gcg atc ttc caa gcc gca aca caa atc caa gaa   259
Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala Thr Gln Ile Gln Glu
         40                  45                  50

cag acc ttc gct ttt gca gtc aaa cta gtc gtg att ttt gga acc tta   307
Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val Ile Phe Gly Thr Leu
     55                  60                  65

atg atc tct gga ggg tgg ctt agc aat atg att tta cgc ttt gca ggt   355
Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile Leu Arg Phe Ala Gly
 70                  75                  80                  85

cag att ttc caa aac ttc tat aaa tgg aaa taaagagctt atgggaatct     405
Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys
                 90                  95

ctctaccaga gctttttttcc aacctaggtt ctgcttactt agattatatc tttcaacatc 465

ctccggccta tgtttggtca gtttttcttc tttta                           500
```

<210> 14
<211> 552
<212> PRT
<213> Chlamydia pneumoniae

<400> 14

```
Met Val Ser Ser Pro Ile Leu Asn Val Pro Leu Lys Asn His Ala Ser
  1               5                  10                  15

Val Ser Gly Lys Phe Thr His Arg Glu Val Ser Lys Leu Ala Ser Asp
             20                  25                  30

Leu Lys Ser Gly Ala Met Ser Phe Val Pro Glu Val Leu Ser Glu Glu
         35                  40                  45

Thr Ile Ser Ser Asp Leu Gly Lys Lys Gln Cys Thr Gln Gly Ile Ile
     50                  55                  60

Ser Ala Cys Cys Gly Leu Ala Met Leu Ile Val Leu Met Ser Val Tyr
 65                  70                  75                  80

Tyr Arg Phe Gly Gly Val Ile Ala Ser Gly Ala Val Leu Leu Asn Leu
                 85                  90                  95

Leu Leu Ile Trp Ala Ala Leu Gln Tyr Leu Asp Ala Pro Leu Thr Leu
            100                 105                 110
```

Ser Gly Leu Ala Gly Ile Val Leu Ala Met Gly Met Ala Val Asp Ala
115 120 125

Asn Val Leu Val Phe Glu Arg Ile Arg Glu Glu Phe Leu Leu Ser Gln
130 135 140

Ser Leu Lys Lys Ser Val Glu Lys Gly Tyr Thr Lys Ala Phe Gly Ala
145 150 155 160

Ile Phe Asp Ser Asn Leu Thr Thr Val Leu Ala Ser Ala Leu Leu Phe
165 170 175

Phe Leu Asp Thr Gly Pro Ile Lys Gly Phe Ala Leu Thr Leu Ile Leu
180 185 190

Gly Ile Phe Ser Ser Met Phe Thr Ala Leu Phe Met Thr Lys Phe Phe
195 200 205

Phe Met Leu Trp Met Asn Lys Thr Gln His Thr Gln Leu His Met Met
210 215 220

Asn Lys Phe Val Gly Ile Lys His Asp Phe Leu Arg Gly Cys Lys Lys
225 230 235 240

Leu Trp Ala Val Ser Gly Ser Val Phe Leu Leu Gly Cys Val Ala Leu
245 250 255

Gly Phe Gly Ala Trp Asn Ser Val Leu Gly Met Asp Phe Lys Gly Gly
260 265 270

Tyr Ala Phe Thr Phe Asn Pro Lys Glu His Gly Ile Ser Asp Val Ala
275 280 285

Gln Met Arg Gly Lys Val Val His Lys Leu Gln Glu Ala Gly Leu Ser
290 295 300

Ser Arg Asp Phe Arg Ile Gln Thr Phe Gly Ser Ser Glu Lys Ile Lys
305 310 315 320

Ile Tyr Phe Ser Asp Lys Ala Leu Ser Tyr Thr Lys Gln Ile Arg Ala
325 330 335

Ser Leu Leu Lys Leu Thr Ile Met Ser Trp Arg Tyr Cys Gly Ile Val
340 345 350

Val Arg Asn Arg Pro Arg Phe Leu Tyr Gly Asn Ser Lys Arg Asn Ala
355 360 365

Lys Phe Trp Ser Lys Val Ser Ser Lys Leu Ser Lys Lys Met Arg Tyr
370 375 380

Gln Ala Thr Ile Gly Leu Leu Gly Ala Leu Ala Ile Ile Leu Leu Tyr
385 390 395 400

```
Val Ser Leu Arg Phe Glu Trp Gln Tyr Ala Phe Ser Ala Val Cys Ala
                405                 410                 415

Leu Ile His Asp Leu Leu Ala Thr Cys Ala Val Leu Phe Ile Ala His
            420                 425                 430

Phe Phe Leu Lys Lys Ile Gln Ile Asp Leu Gln Ala Ile Gly Ala Leu
        435                 440                 445

Met Thr Val Leu Gly Tyr Ser Leu Asn Asn Thr Leu Ile Ile Phe Asp
    450                 455                 460

Arg Ile Arg Glu Asp Arg Gln Ala Asn Leu Phe Thr Pro Met His Val
465                 470                 475                 480

Leu Val Asn Asp Ala Leu Gln Lys Thr Phe Ser Arg Thr Val Met Thr
                485                 490                 495

Thr Ala Thr Thr Leu Ser Val Leu Leu Met Leu Leu Phe Ile Gly Gly
            500                 505                 510

Ser Ser Val Phe Asn Phe Ala Phe Ile Met Thr Ile Gly Ile Leu Leu
        515                 520                 525

Gly Thr Leu Ser Ser Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met
    530                 535                 540

Val Arg Lys Glu Asn Arg Ser Lys
545                 550


<210> 15
<211> 196
<212> PRT
<213> Chlamydia pneumoniae

<400> 15
Met Ser Ser Asn Leu His Pro Val Gly Gly Thr Gly Thr Gly Ala Ala
  1               5                  10                  15

Ala Pro Glu Ser Val Leu Asn Ile Val Glu Glu Ile Ala Ala Ser Gly
            20                  25                  30

Ser Val Thr Ala Gly Leu Gln Ala Ile Thr Ser Ser Pro Gly Met Val
        35                  40                  45

Asn Leu Leu Ile Gly Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg
    50                  55                  60

Glu Ser Lys Leu Phe Gln Ser Arg Ala Cys Gln Ile Thr Leu Leu Val
65                  70                  75                  80

Leu Gly Ile Leu Leu Val Val Ala Gly Leu Ala Cys Met Phe Ile Phe
                85                  90                  95
```

His Ser Gln Leu Gly Ala Asn Ala Phe Trp Leu Ile Ile Pro Ala Ala
100 105 110

Ile Gly Leu Ile Lys Leu Leu Val Thr Ser Leu Cys Phe Asp Glu Ala
115 120 125

Cys Thr Ser Glu Lys Leu Met Val Phe Gln Lys Trp Ala Gly Val Leu
130 135 140

Glu Asp Gln Leu Asp Asp Gly Ile Leu Asn Asn Ser Asn Lys Ile Phe
145 150 155 160

Gly His Val Lys Thr Glu Gly Asn Thr Ser Arg Ala Thr Thr Pro Val
165 170 175

Leu Asn Asp Gly Arg Gly Thr Pro Val Leu Ser Pro Leu Val Ser Lys
180 185 190

Ile Ala Arg Val
195

<210> 16
<211> 245
<212> PRT
<213> Chlamydia pneumoniae

<400> 16
Met Thr Ile Arg Ile Leu Ala Glu Gly Leu Ala Phe Arg Tyr Gly Ser
1 5 10 15

Lys Gly Pro Asn Ile Ile His Asp Val Ser Phe Ser Val Tyr Asp Gly
20 25 30

Asp Phe Ile Gly Ile Ile Gly Pro Asn Gly Gly Gly Lys Ser Thr Leu
35 40 45

Thr Met Leu Ile Leu Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys
50 55 60

Thr Phe Pro Ser His Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly
65 70 75 80

Trp Val Pro Gln His Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val
85 90 95

Lys Asp Val Val Leu Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly
100 105 110

Lys Tyr Lys Lys Lys Asp Phe Glu Ala Val Asp His Ala Leu Asp Leu
115 120 125

Val Gly Leu Ser Asp Thr Thr Thr Thr Ala Phe Ala His Leu Ser Gly
130 135 140

Gly Gln Ile Gln Arg Val Leu Leu Ala Arg Ala Leu Ala Ser Tyr Pro
145 150 155 160

```
Glu Ile Leu Ile Leu Asp Glu Pro Thr Thr Asn Ile Asp Pro Asp Asn
                165                 170                 175

Gln Gln Arg Ile Leu Ser Ile Leu Lys Lys Leu Asn Arg Thr Cys Thr
            180                 185                 190

Ile Leu Met Val Thr His Asp Leu His His Thr Thr Asn Tyr Phe Asn
        195                 200                 205

Lys Val Phe Tyr Met Asn Lys Thr Leu His Phe Ile Gly Arg His Phe
    210                 215                 220

Asp Leu Asn Arg Pro Ile Leu Leu Ser Ser Tyr Lys Asn Gln Glu Phe
225                 230                 235                 240

Ser Cys Ser Pro His
                245
```


<210> 17
<211> 278
<212> PRT
<213> Chlamydia pneumoniae

<400> 17

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Met His Lys Val Ile Val Phe Ile Phe Leu Thr Leu Tyr Ser Leu Lys
  1               5                  10                  15

Ser Tyr Gly Asn Asp Val Ile Asp Lys Pro His Val Leu Val Ser Ile
            20                  25                  30

Ala Pro Tyr Lys Phe Leu Val Glu Gln Ile Ala Glu Glu Thr Cys Phe
        35                  40                  45

Val Tyr Ala Ile Val Thr Asn His Tyr Asp Pro His Thr Tyr Glu Leu
    50                  55                  60

Pro Pro Gln Gln Ile Lys Glu Leu Arg Gln Gly Asp Leu Trp Phe Arg
65                  70                  75                  80

Ile Gly Glu Ala Phe Gly Lys Asn Leu Leu Glu Lys Pro Tyr Met Gln
                85                  90                  95

Gln Val Asp Leu Ser Gln Asn Val Ser Leu Ile Gln Gly Lys Pro Cys
            100                 105                 110

Cys Asn Gln His Thr Thr Asn Tyr Asp Thr His Thr Trp Leu Ser Pro
        115                 120                 125

Lys Asn Leu Lys Val Gln Val Glu Thr Ile Val Thr Thr Leu Ser Lys
    130                 135                 140
```

Lys Tyr Pro Gln His Ala Thr Leu Tyr Gln Ser Asn Gly Glu Lys Leu
145 150 155 160

Leu Leu Ala Leu Asp Gln Leu Asn Glu Glu Ile Leu Thr Ile Thr Ser
165 170 175

Lys Ala Lys Gln Arg His Ile Leu Val Ser His Gly Ala Phe Gly Tyr
180 185 190

Phe Cys Arg Asp Tyr Asn Phe Ser Gln His Thr Ile Glu Lys Ser Ser
195 200 205

His Val Glu Pro Ser Pro Lys Asp Val Ala Arg Val Phe Arg Asp Ile
210 215 220

Glu Gln Tyr Lys Ile Ser Ser Val Ile Leu Leu Glu Tyr Ser Gly Arg
225 230 235 240

Arg Ser Ser Ala Met Leu Ala Asp Arg Phe His Met His Thr Val Asn
245 250 255

Leu Asp Pro Tyr Ala Glu Asn Val Leu Val Asn Leu Lys Thr Ile Ala
260 265 270

Thr Thr Phe Ser Ser Leu
275

<210> 18
<211> 469
<212> PRT
<213> Chlamydia pneumoniae

<400> 18
Met Gly Pro Gly Ser Val Leu Ser Asn His Ser Lys Glu Ala Gly Gly
1 5 10 15

Ile Ala Ile Asn Asn Val Ile Ile Asp Phe Ser Glu Ile Val Pro Thr
20 25 30

Lys Asp Asn Ala Thr Val Ala Pro Pro Thr Leu Lys Leu Val Ser Arg
35 40 45

Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp Ile Thr Gly Thr Val Thr
50 55 60

Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln Asn Ser Tyr Leu Gly Glu
65 70 75 80

Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp Asn Ser Ala Ser Gly Ala
85 90 95

Val Thr Ala Thr Asn Val Thr Leu Gln Gly Asn Leu Gly Ala Lys Lys
100 105 110

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Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro Asn Ser Ser Gly Ser Lys
        115                 120                 125

Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr Leu Arg Trp Pro Tyr Ile
    130                 135                 140

Pro Arg Asp Asn His Phe Tyr Ile Asn Ser Ile Trp Gly Ala Gln Asn
145                 150                 155                 160

Ser Leu Val Thr Val Asn Gln Gly Ile Leu Gly Asn Met Leu Asn Asn
                165                 170                 175

Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn Phe Trp Ala Ser Ala Ile
            180                 185                 190

Gly Ser Phe Leu Arg Lys Glu Val Ser Arg Asn Ser Asp Ser Phe Thr
        195                 200                 205

Tyr His Gly Arg Gly Tyr Thr Ala Ala Val Asp Ala Lys Pro Arg Gln
    210                 215                 220

Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln Val Phe Gly His Ala Glu
225                 230                 235                 240

Ser Glu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly His Ser
                245                 250                 255

Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile Phe Tyr Phe Pro Ala Ile
            260                 265                 270

Arg Ser Arg Pro Ile Leu Phe Gln Gly Val Ala Thr Tyr Gly Tyr Met
        275                 280                 285

Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser Ile Glu Glu Lys Asn Met
    290                 295                 300

Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe Asp Leu Arg Phe Ser Val
305                 310                 315                 320

Asp Leu Lys Glu Pro Gln Pro His Ser Thr Ala Arg Leu Thr Phe Tyr
                325                 330                 335

Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln Glu Lys Phe Thr Glu Leu
            340                 345                 350

Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys Ser Tyr Gly Asn Leu Ala
        355                 360                 365

Ile Pro Thr Gly Phe Ser Val Asp Gly Ala Leu Ala Trp Arg Glu Ile
    370                 375                 380

Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr Leu Pro Val Ile Leu Arg
385                 390                 395                 400
```

```
Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu Ser Thr Lys Glu Lys Gly
                405                 410                 415

Asn Val Val Asn Val Leu Pro Thr Arg Asn Ala Ala Arg Ala Glu Val
            420                 425                 430

Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp Thr Leu Tyr Gly Thr Tyr
        435                 440                 445

Thr Ile Asp Ala Ser Met Asn Thr Leu Val Gln Met Ala Asn Gly Gly
    450                 455                 460

Ile Arg Phe Val Phe
465
```

<210> 19
<211> 922
<212> PRT
<213> Chlamydia pneumoniae

<400> 19

```
Met Arg Phe Ser Leu Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu
  1               5                  10                  15

Leu Ser Val Phe Asp Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr
            20                  25                  30

Pro Glu Asp Ser Phe His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr
        35                  40                  45

Asn Val Gln Ala Gly Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile
    50                  55                  60

Ser Asn Val Asp Asn Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr
65                  70                  75                  80

Ser Gly Ser Val Thr Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn
                85                  90                  95

Asn Ile Ser Ser Gly Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln
            100                 105                 110

Asp Pro Gln Ala Thr Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe
        115                 120                 125

Ile Gln Ser Pro Gly Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys
    130                 135                 140

Asn Ala Leu Met Leu Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn
145                 150                 155                 160

Gln Ser Lys Thr Lys Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile
                165                 170                 175
```

```
Val Gly Asn Tyr Asp Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe
            180                 185                 190

Gly Gly Ala Ile His Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln
        195                 200                 205

Ala Glu Ile Arg Phe Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly
    210                 215                 220

Ala Leu Tyr Ser Asp Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val
225                 230                 235                 240

Leu Phe Arg Glu Asn Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly
                245                 250                 255

Ala Val Cys Cys Leu Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile
            260                 265                 270

Val Thr Phe Ser Asp Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser
        275                 280                 285

Ile Met Gly Gly Gly Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser
    290                 295                 300

Gly Gly Pro Thr Leu Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln
305                 310                 315                 320

Asn Leu Gly Gly Ala Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu
                325                 330                 335

Ser Ala Glu Lys Gly Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu
            340                 345                 350

Pro Phe Leu Asn Gly Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys
        355                 360                 365

Leu Gln Ala Arg Asn Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr
    370                 375                 380

Ser Glu Ala Asp Gly Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys
385                 390                 395                 400

Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu
                405                 410                 415

Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn
            420                 425                 430

Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val
        435                 440                 445

Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly
    450                 455                 460

Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala
465                 470                 475                 480
```

Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys
485 490 495

Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu
500 505 510

Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser
515 520 525

Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val
530 535 540

Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe
545 550 555 560

Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly
565 570 575

Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu
580 585 590

Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg
595 600 605

Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp
610 615 620

Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala
625 630 635 640

Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu
645 650 655

Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe
660 665 670

Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu
675 680 685

Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu
690 695 700

Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly
705 710 715 720

Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe
725 730 735

Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala
740 745 750

Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile
755 760 765

Glu Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu
770 775 780

Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr
785 790 795 800

His Gly Asp Phe Lys Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn
805 810 815

Gly Ser Leu Thr Ser Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys
820 825 830

Leu Ala Leu Ser Gln Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile
835 840 845

Pro Asp Ile Phe Arg Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile
850 855 860

Ser Gly Asp Ser Trp Leu Val Pro Ala Ala His Val Ser Arg His Ala
865 870 875 880

Phe Val Gly Ser Gly Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu
885 890 895

Leu Leu Cys Arg Gly Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr
900 905 910

Asn Ile Asn Cys Gly Ser Lys Phe Arg Phe
915 920

<210> 20
<211> 375
<212> PRT
<213> Chlamydia pneumoniae

<400> 20
Met Pro Ser Ser Trp Lys Arg Leu Leu Gln Val Leu Ser His Lys Ile
1 5 10 15

Ala Ala Thr Glu Ser Gly Gly Gly Ile Tyr Ala Lys Asp Ile Gln Leu
20 25 30

Gln Ala Leu Pro Gly Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr
35 40 45

Ser Leu Thr Thr Ser Thr Asn Leu Tyr Gly Gly Gly Ile Tyr Ser Ser
50 55 60

Gly Ala Val Thr Leu Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly
65 70 75 80

Asn Ser Val Ile Asn Thr Ala Thr Ser Gln Asp Ala Asp Ile Gln Gly
85 90 95

```
Gly Gly Ile Tyr Ala Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr
            100                 105                 110

Pro Ile Leu Phe Ser Asn Asn Ser Ala Ala Thr Lys Lys Thr Ser Thr
        115                 120                 125

Thr Lys Gln Ile Ala Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile
    130                 135                 140

Glu Asn Asn Ser Gln Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser
145                 150                 155                 160

Glu Ala Thr Thr Ala Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly
                165                 170                 175

Ala Ile Ala Ala Asn Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr
            180                 185                 190

Phe Lys Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp
        195                 200                 205

Leu Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly
    210                 215                 220

Ser Val Leu Phe Gln Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile
225                 230                 235                 240

Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly
                245                 250                 255

Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu
            260                 265                 270

Thr Leu Ala Pro Asn Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr
        275                 280                 285

Glu Thr Thr Ala Thr Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala
    290                 295                 300

Ile Tyr Gly Asn Asn Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala
305                 310                 315                 320

Glu Asn Gly Ser Ile Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn
                325                 330                 335

Lys Tyr Cys Ser Ile Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala
            340                 345                 350

Ser Ala Gly Lys Ala Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro
        355                 360                 365

Lys Lys Gln Leu Leu Lys Ser
    370                 375
```

<210> 21
<211> 871
<212> PRT
<213> Chlamydia pneumoniae

<400> 21

```
Met Lys Tyr Ser Leu Pro Trp Leu Leu Thr Ser Ser Ala Leu Val Phe
  1               5                  10                  15

Ser Leu His Pro Leu Met Ala Ala Asn Thr Asp Leu Ser Ser Ser Asp
             20                  25                  30

Asn Tyr Glu Asn Gly Ser Ser Gly Ser Ala Ala Phe Thr Ala Lys Glu
         35                  40                  45

Thr Ser Asp Ala Ser Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser
     50                  55                  60

Ile Thr Asn Val Ser Ala Ile Thr Pro Ala Asp Lys Ser Cys Phe Thr
 65                  70                  75                  80

Asn Thr Gly Gly Ala Leu Ser Phe Val Gly Ala Asp His Ser Leu Val
                 85                  90                  95

Leu Gln Thr Ile Ala Leu Thr His Asp Gly Ala Ala Ile Asn Asn Thr
            100                 105                 110

Asn Thr Ala Leu Ser Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser
        115                 120                 125

Ala Pro Ala Thr Gly Thr Ser Gly Gly Lys Gly Ala Ile Cys Val Thr
    130                 135                 140

Asn Thr Glu Gly Gly Thr Ala Thr Phe Thr Asp Asn Ala Ser Val Thr
145                 150                 155                 160

Leu Gln Lys Asn Thr Ser Glu Lys Asp Gly Ala Ala Val Ser Ala Tyr
                165                 170                 175

Ser Ile Asp Leu Ala Lys Thr Thr Thr Ala Ala Leu Leu Asp Gln Asn
            180                 185                 190

Thr Ser Thr Lys Asn Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr
        195                 200                 205

Val Gln Gly Asn Ser Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr
    210                 215                 220

Asp Lys Gly Gly Gly Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp
225                 230                 235                 240

Ala Asn Thr Gly Val Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly
                245                 250                 255

Gly Ala Trp Ser Ser Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln
            260                 265                 270
```

```
Val Leu Phe Gln Glu Asn Lys Thr Thr Gly Ser Ala Ala Gln Ala Asn
        275                 280                 285

Asn Pro Glu Gly Cys Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala
    290                 295                 300

Thr Asp Lys Thr Gly Leu Ala Ile Ser Gln Asn Gln Glu Met Ser Phe
305                 310                 315                 320

Thr Ser Asn Thr Thr Thr Ala Asn Gly Gly Ala Ile Tyr Ala Thr Lys
                325                 330                 335

Cys Thr Leu Asp Gly Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala
            340                 345                 350

Thr Ala Gly Cys Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser
        355                 360                 365

Leu Lys Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys
    370                 375                 380

Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn
385                 390                 395                 400

Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser
                405                 410                 415

Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ala Phe Ile Asp
            420                 425                 430

Ser Gly Ser Val Ser Asp Lys Thr Gly Leu Ser Ile Ala Asn Asn Gln
        435                 440                 445

Glu Val Ser Leu Thr Ser Asn Ala Ala Thr Val Ser Gly Gly Ala Ile
    450                 455                 460

Tyr Ala Thr Lys Cys Thr Leu Thr Gly Asn Gly Ser Leu Thr Phe Asp
465                 470                 475                 480

Gly Asn Thr Ala Gly Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu
                485                 490                 495

Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn
            500                 505                 510

Thr Ala Lys Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu
        515                 520                 525

Ser Gly Asn Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro
    530                 535                 540

Ser Asn Ser Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser
545                 550                 555                 560
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Phe Leu Glu Ser Ala Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu
565 570 575

Asp Asn Glu Asn Val Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly
580 585 590

Gly Ala Ile Tyr Ala Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu
595 600 605

Thr Phe Asp Gly Asn Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr
610 615 620

Glu Thr Glu Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe
625 630 635 640

Ser Thr Asn Thr Ala Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn
645 650 655

Thr Ser Phe Thr Lys Asn Lys Ala Leu Val Phe Ser Gly Asn Ser Ala
660 665 670

Thr Ala Thr Ala Thr Thr Thr Thr Asp Gln Glu Gly Cys Gly Gly Ala
675 680 685

Ile Leu Cys Asn Ile Ser Glu Ser Asp Ile Ala Thr Lys Ser Leu Thr
690 695 700

Leu Thr Glu Asn Glu Ser Leu Ser Phe Ile Asn Asn Thr Ala Lys Arg
705 710 715 720

Ser Gly Gly Gly Ile Tyr Ala Pro Lys Cys Val Ile Ser Gly Ser Glu
725 730 735

Ser Ile Asn Phe Asp Gly Asn Thr Ala Glu Thr Ser Gly Gly Ala Ile
740 745 750

Tyr Ser Lys Asn Leu Ser Ile Thr Ala Asn Gly Pro Val Ser Phe Thr
755 760 765

Asn Asn Ser Gly Gly Lys Gly Gly Ala Ile Tyr Ile Ala Asp Ser Gly
770 775 780

Glu Leu Ser Leu Glu Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn
785 790 795 800

Arg Ala Thr Glu Gly Thr Ser Thr Pro Asn Ser Ile His Leu Gly Ala
805 810 815

Arg Gly Lys Ile Thr Lys Leu Ala Ala Ala Pro Gly His Thr Ile Tyr
820 825 830

Phe Tyr Asp Pro Ile Thr Met Glu Ala Pro Ala Ser Gly Gly Thr Ile
835 840 845

Glu Glu Leu Val Ile Asn Pro Val Val Lys Ala Ile Val Pro Pro Pro
850 855 860

Gln Pro Lys Asn Gly Pro Ile
865 870

<210> 22
<211> 963
<212> PRT
<213> Chlamydia pneumoniae

<400> 22
Met Thr Asn Ser Ile Phe Ile Ser Lys Phe Gly Cys Leu Cys Asp Pro
1 5 10 15

Phe Val Ser Ala Phe Tyr Pro Thr Ala Leu Cys Cys Ser Leu Ser Gly
20 25 30

Asn Glu Val Pro Asn Leu Ala Ser Cys Gln Met Ser Arg Lys Asp Ile
35 40 45

Ser Ala Phe His Thr Ser Pro Ser Phe Arg Leu Asn Val Thr Pro Glu
50 55 60

Pro Leu Val Ser Ser Phe Arg Pro Ser Asn Leu Leu Asn Gly Phe Gly
65 70 75 80

His Asp Ile Thr Gln Asp Ile Thr Ile Thr Gly Asn Ser Ile Asn Ser
85 90 95

Val Ile Asp Tyr Asn Tyr His Tyr Glu Asp Gly Gly Ile Leu Ala Cys
100 105 110

Lys Asn Leu Phe Ile Ser Glu Asn Lys Gly Asn Leu Ser Phe Glu Arg
115 120 125

Asn Ser Ser His Ser Ser Gly Gly Ala Leu Tyr Ser Val Arg Glu Cys
130 135 140

Trp Ile Ser Lys Asn Gln Asn Tyr Ser Phe Ile Ser Asn Ala Ala Ser
145 150 155 160

Leu Ala Thr Thr Thr Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu
165 170 175

Asp Ser Tyr Ile Thr Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn
180 185 190

Val Ser Lys Asn Arg Gly Gly Ala Ile Tyr Val Gly Val Ser Leu Ser
195 200 205

Ile Thr Asp Asn Leu Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu
210 215 220

Glu Asp Ser Ser Phe Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile
225 230 235 240

Glu Arg Asn Tyr Gln Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln
245 250 255

Gly Val Val Tyr Phe Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys
260 265 270

Glu Ile Ile Glu Ile Ser Asn His Ser Ala Ser Ser Ile Asn Thr Ala
275 280 285

Ser Gly Lys Leu Tyr Pro Gly Gly Gly Gly Ile Met Cys Thr Ser Leu
290 295 300

Ser His Glu Asn Asn Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala
305 310 315 320

Ala Leu Ser Gly Gly Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile
325 330 335

Thr Val Arg Thr Ala Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala
340 345 350

Leu Ile Asn Leu Ser Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu
355 360 365

Ser Ala Asp Tyr Gly Asp Ile Leu Phe Asn Asn Asn Thr Ile Thr Ser
370 375 380

Ser Ser Pro Gln Pro Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly
385 390 395 400

Ile Asn Leu Lys Leu Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr
405 410 415

Asp Pro Ile Asp His Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn
420 425 430

Tyr Glu Pro His His Leu Gly Thr Val Leu Phe Ser Gly Ile Asn Val
435 440 445

Asp Ser Asn Ala Thr Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn
450 455 460

Ser Ser Arg Leu Glu Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala
465 470 475 480

Ile Ser Cys Lys Thr Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly
485 490 495

Asn Ala Ala Leu Ile Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe
500 505 510

Asn Ala Ile Ala Ile Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser
515 520 525

Ala Pro Lys Phe Trp Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser
530 535 540

Glu Asp Thr Ser Ser Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu
545 550 555 560

Asn Asp Glu Asn Glu Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro
565 570 575

Arg Lys Asp Ile Pro Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys
580 585 590

Ile Asp Thr Ser Asn Leu Ile Val Glu Ala Met Asn Leu Asp Glu His
595 600 605

Tyr Gly Tyr Gln Gly Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr
610 615 620

Thr Thr Ser Ser Thr Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln
625 630 635 640

Leu Tyr Val Asp Trp Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg
645 650 655

His Gly Glu Phe Ile Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala
660 665 670

Leu Leu Gly Ile Arg Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp
675 680 685

Leu Glu Ala Ser Leu Gln Gly Leu Gly Leu Leu Ile Asn Gln His Asn
690 695 700

Arg Glu Gly Arg Lys Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala
705 710 715 720

Thr Thr Ser Ala Lys Thr Ala Ala Arg His Ser Phe Ser Leu Gly Phe
725 730 735

Ala Gln Met Phe Ser Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr
740 745 750

Ser Ser His Asn Tyr Phe Ala Gly Leu Arg Phe Asp Ser Leu Leu Phe
755 760 765

Arg Asp Phe Ile Ser Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp
770 775 780

His His Met Leu Cys His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys
785 790 795 800

Ala Phe Phe Asn Asn His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe
805 810 815

Leu Pro Ala Arg Ile Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser
820 825 830

Ala Ile Ala Leu Arg Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp
835 840 845

His Ile Arg Lys Phe His Pro Lys His Pro Leu Thr Asp Leu Ser Ser
850 855 860

Pro Ile Gly Phe Arg Ser Glu Trp Lys Thr Ser His His Ile Pro Met
865 870 875 880

Leu Trp Thr Thr Glu Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn
885 890 895

Pro Glu Met Phe Thr Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr
900 905 910

Gln Ala Thr Pro Val Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn
915 920 925

Thr Ser Gln Leu Phe Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala
930 935 940

Gln Val Ser Ser Ser Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His
945 950 955 960

Cys Thr Phe

<210> 23
<211> 514
<212> PRT
<213> Chlamydia pneumoniae

<400> 23
Met Thr Ile Leu Arg Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala
1 5 10 15

Leu Pro Ala Ala Ala Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr
20 25 30

Asn Gly Ala Ile Asn Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr
35 40 45

Pro Glu Gly Thr Ser Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn
50 55 60

Val Lys His Asp Gln Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly
65 70 75 80

Asn Leu Phe Phe Met Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu
85 90 95

Met Thr Glu Gly Phe Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr
100 105 110

```
Thr Leu Thr Leu Ser Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro
        115                 120                 125

Leu Leu Pro Gln Gly Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met
    130                 135                 140

Ile Glu Asn Ser Glu Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp
145                 150                 155                 160

Ser Gly Ala Ala Ile Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser
                165                 170                 175

Arg Pro Ser Val Asn Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp
            180                 185                 190

Asn Val Ser Gln Val Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr
        195                 200                 205

Leu Thr Thr Arg Gly Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His
    210                 215                 220

Asp Val Asn Ser Asn Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser
225                 230                 235                 240

Ile Ser Ile Ser Val Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr
                245                 250                 255

Ala Ser Gln Asp Gly Asn Thr Ile His Asn Ser Ile His Leu Gln Ser
            260                 265                 270

Gly Ala Gln Phe Lys Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr
        275                 280                 285

Phe Tyr Asp Pro Ile Ser His Ser Glu Ser His Lys Ile Thr Asp Leu
    290                 295                 300

Val Ile Asn Ala Pro Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser
305                 310                 315                 320

Phe Ser Gly Leu Cys Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu
                325                 330                 335

Thr Ser Thr Ile Leu Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser
            340                 345                 350

Leu Ser Asp Gly Val Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala
        355                 360                 365

Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly
    370                 375                 380

Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn
385                 390                 395                 400

Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser
                405                 410                 415
```

```
Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp
            420                 425                 430

Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu
        435                 440                 445

Gly Pro Ser Phe Asp Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg
    450                 455                 460

Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu
465                 470                 475                 480

Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr
                485                 490                 495

Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser
            500                 505                 510

Thr Pro


<210> 24
<211> 289
<212> PRT
<213> Chlamydia pneumoniae

<400> 24
Met Gly Ile Ser Leu Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr
  1               5                  10                  15

Leu Asp Tyr Ile Phe Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe
             20                  25                  30

Leu Leu Leu Leu Ala Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe
         35                  40                  45

Leu Gly Ala Lys Leu Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu
     50                  55                  60

Ser Trp Leu Ala Ile Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile
 65                  70                  75                  80

Thr Asn Tyr Met Asp Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu
                85                  90                  95

Met Ile Ile Gly Ile Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr
            100                 105                 110

Ala Ala Gln Ser Ala Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln
        115                 120                 125

Gly Leu Glu Gly Ala Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro
    130                 135                 140
```

```
His Gly Ile Leu Tyr His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val
145                 150                 155                 160

Gly Gly His Arg Ile Val Ile Ser Leu Leu Leu Gln Thr Leu Glu Val
                165                 170                 175

Ile Pro Ile His Ser Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala
            180                 185                 190

Pro Ile Trp Ile Thr Met Ile Lys Met Cys Gln Leu Cys Leu Val Met
        195                 200                 205

Thr Ile Gln Leu Ser Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp
    210                 215                 220

Leu Phe Leu Gly Ile Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile
225                 230                 235                 240

Tyr Leu Leu Ser Ala Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr
                245                 250                 255

Leu Ala Trp Trp Phe Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala
            260                 265                 270

Trp Phe Lys Glu Val Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val
        275                 280                 285

Leu
```


<210> 25
<211> 265
<212> PRT
<213> Chlamydia pneumoniae

<400> 25

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Met Lys His Ser Lys Glu Asp Asp Leu Ser Arg Phe Leu Pro Lys Asn
  1               5                  10                  15

Leu Leu Val Glu Ser Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu
             20                  25                  30

Ser Phe Thr Met Ser Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr
         35                  40                  45

Ile Ala Met Lys Glu Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala
     50                  55                  60

Trp Leu Pro Glu Pro Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly
 65                  70                  75                  80

Ile Ser Ile Ala Pro His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu
                 85                  90                  95

Leu Asp Met Leu Ser Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu
            100                 105                 110
```

```
Ile Phe Leu Pro Ala Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly
        115                 120                 125

Pro Val Lys Ile Ala Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala
    130                 135                 140

Lys Glu Leu Lys His Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys
145                 150                 155                 160

Asn Ala Leu Ser Pro Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser
                165                 170                 175

His Pro Met Lys His Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr
            180                 185                 190

Thr Asp Ala Glu Leu Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe
        195                 200                 205

Leu Gly Lys Ala Leu Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe
    210                 215                 220

Leu Arg Arg Leu Asp Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu
225                 230                 235                 240

Lys Thr Trp Tyr Asp His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu
                245                 250                 255

Glu Gln Cys Met Lys Val Leu Val Lys
            260                 265
```

<210> 26
<211> 95
<212> PRT
<213> Chlamydia pneumoniae

<400> 26

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Met Leu Ala Phe Phe Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr
  1               5                  10                  15

Ser Tyr Gln Ser Leu Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile
            20                  25                  30

Ile Leu Ala Ser Ile Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala
        35                  40                  45

Thr Gln Ile Gln Glu Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val
    50                  55                  60

Ile Phe Gly Thr Leu Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile
65                  70                  75                  80

Leu Arg Phe Ala Gly Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys
                85                  90                  95
```

Figure 1

Restriction enzyme analysis of CPN100686 (RY 54 - SEQ ID NO. 1)

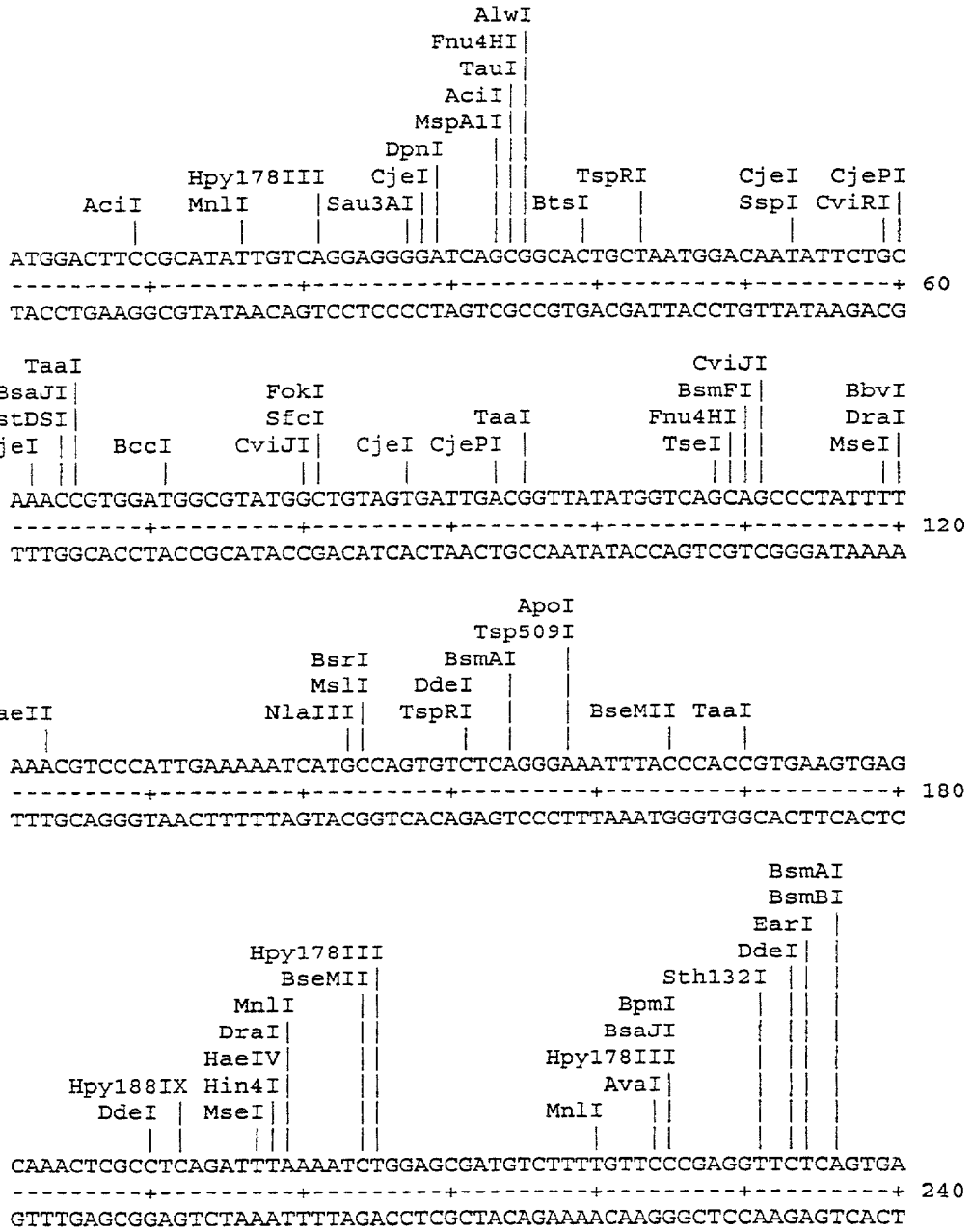


Figure 1 (Continued)

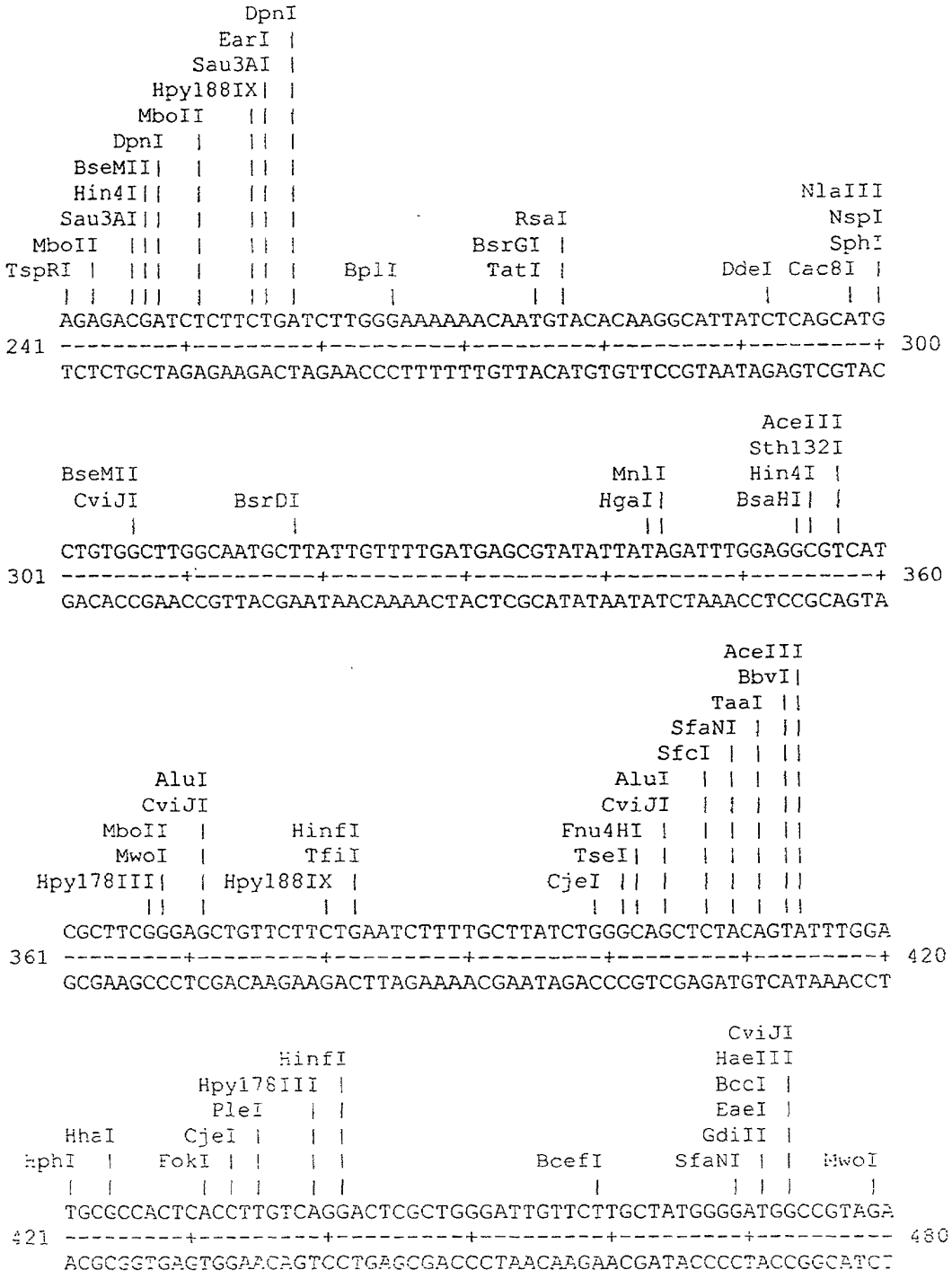


Figure 1 (continued)

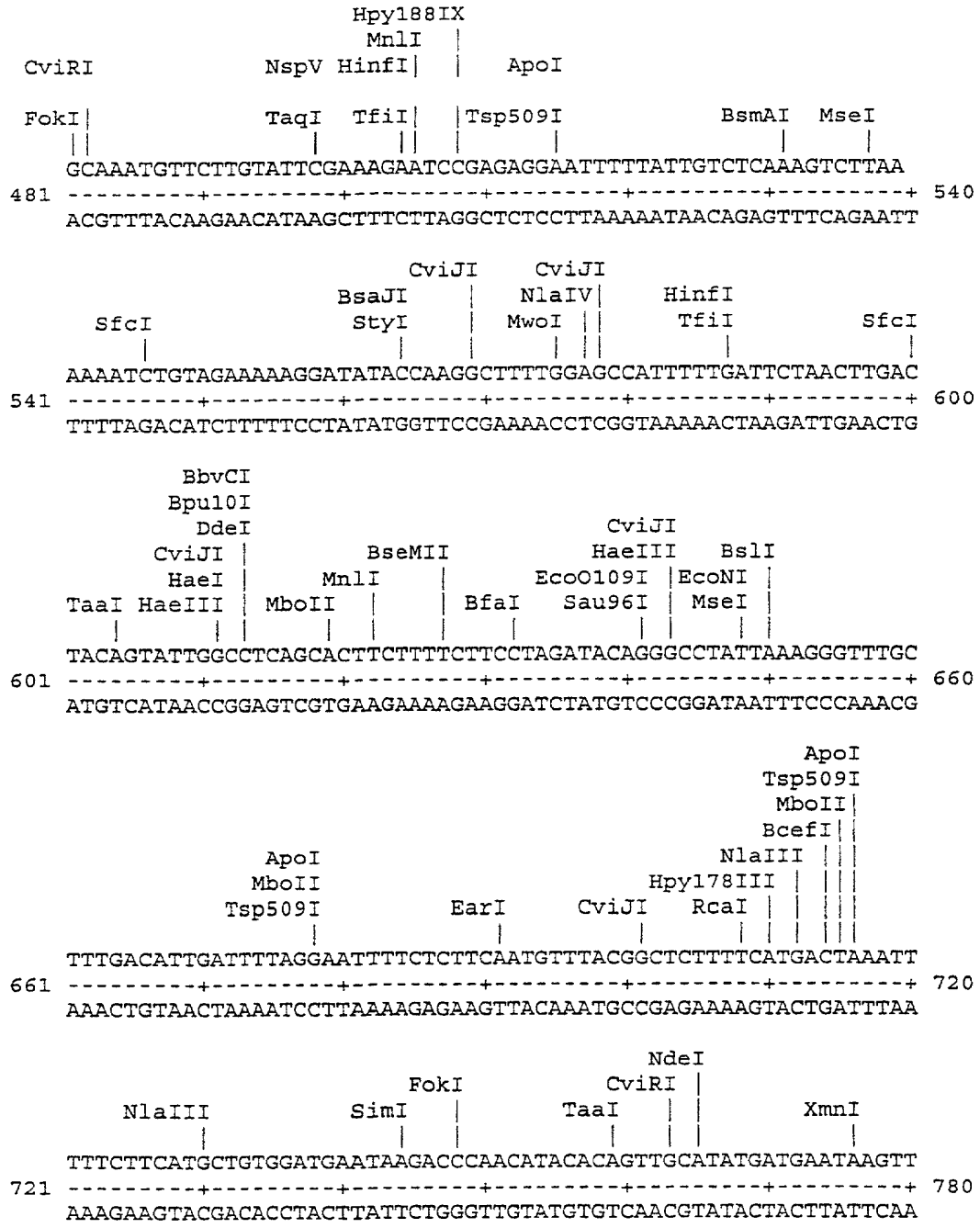


Figure 1 (continued)

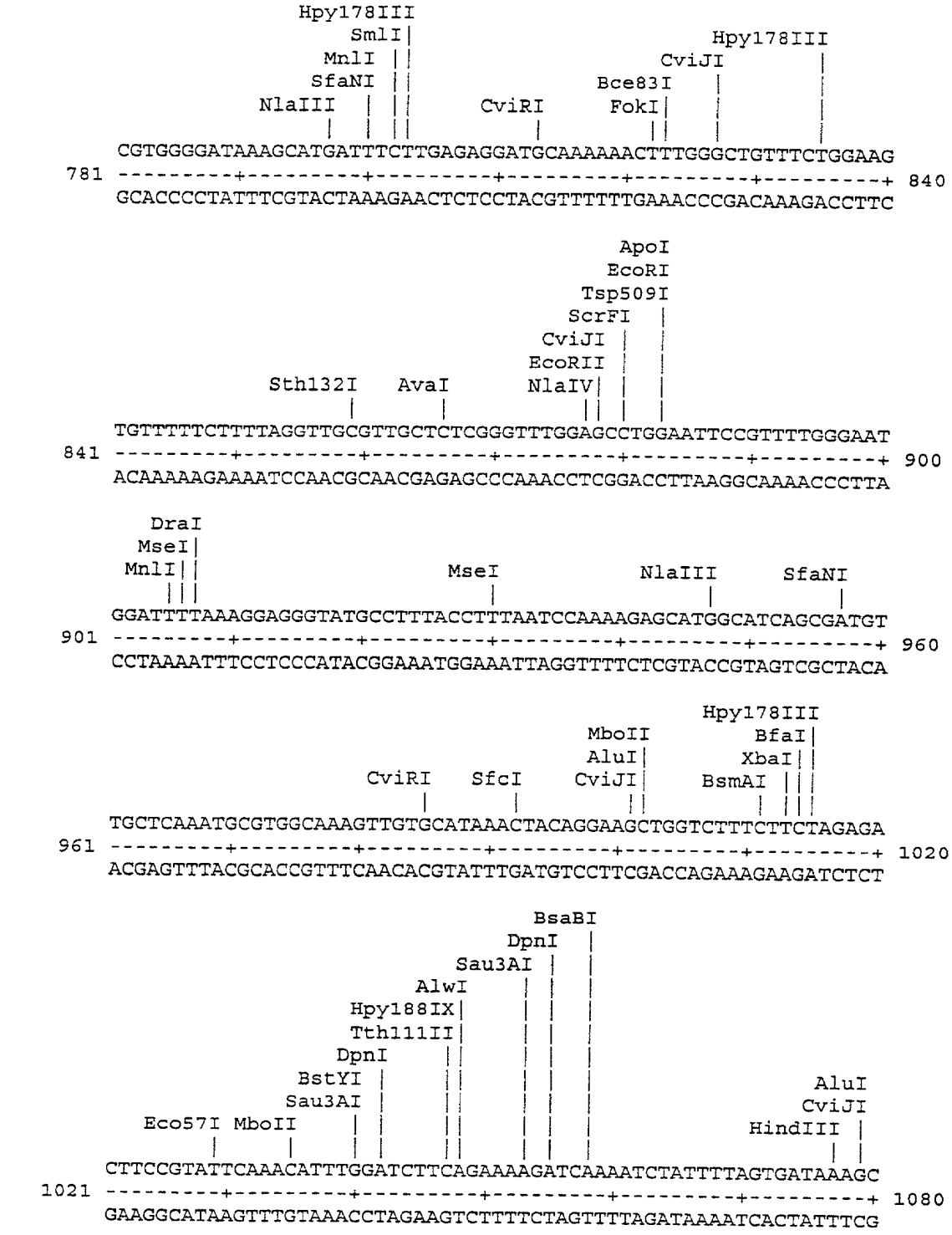


Figure 1 (continued)

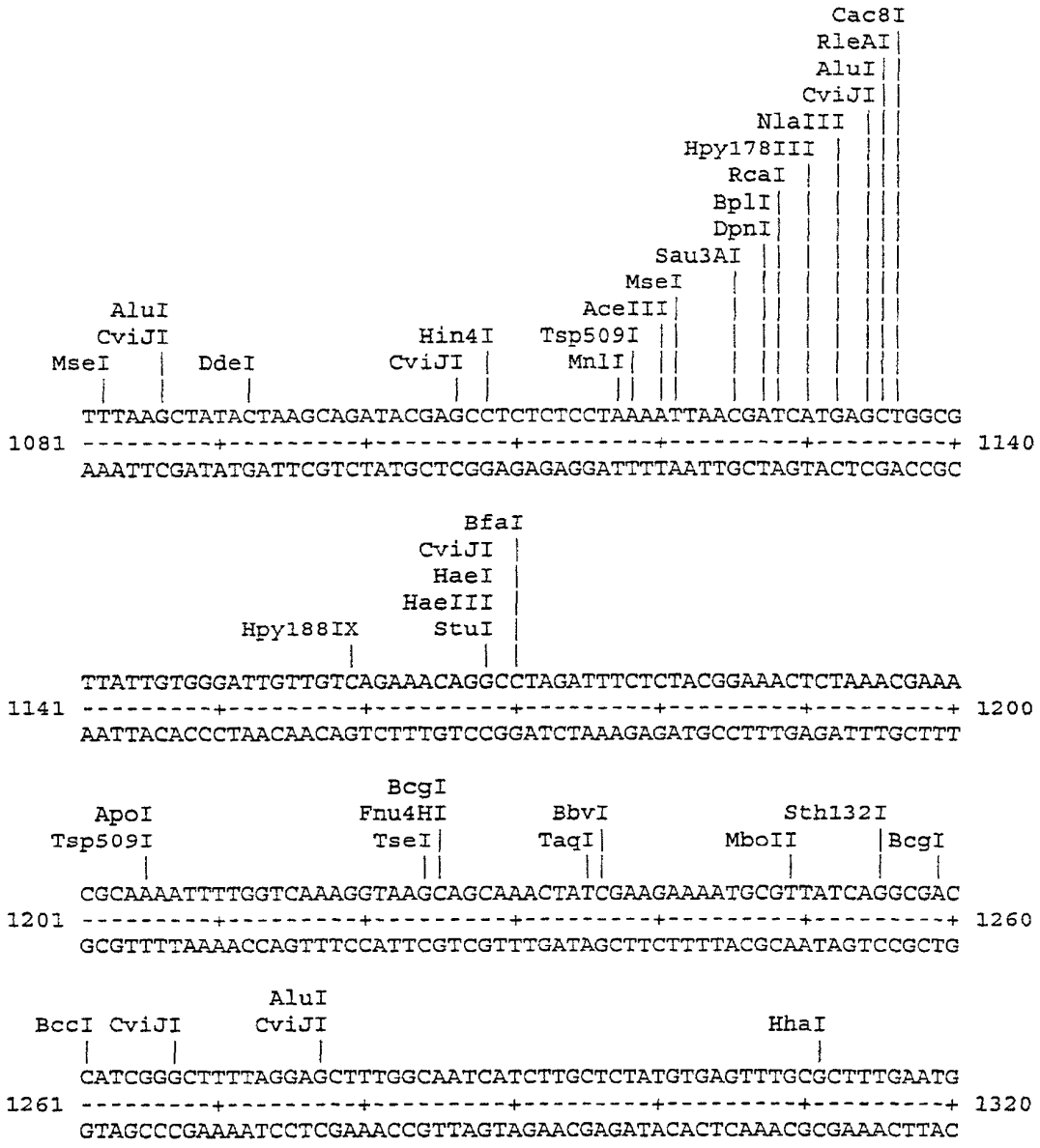


Figure 1 (continued)

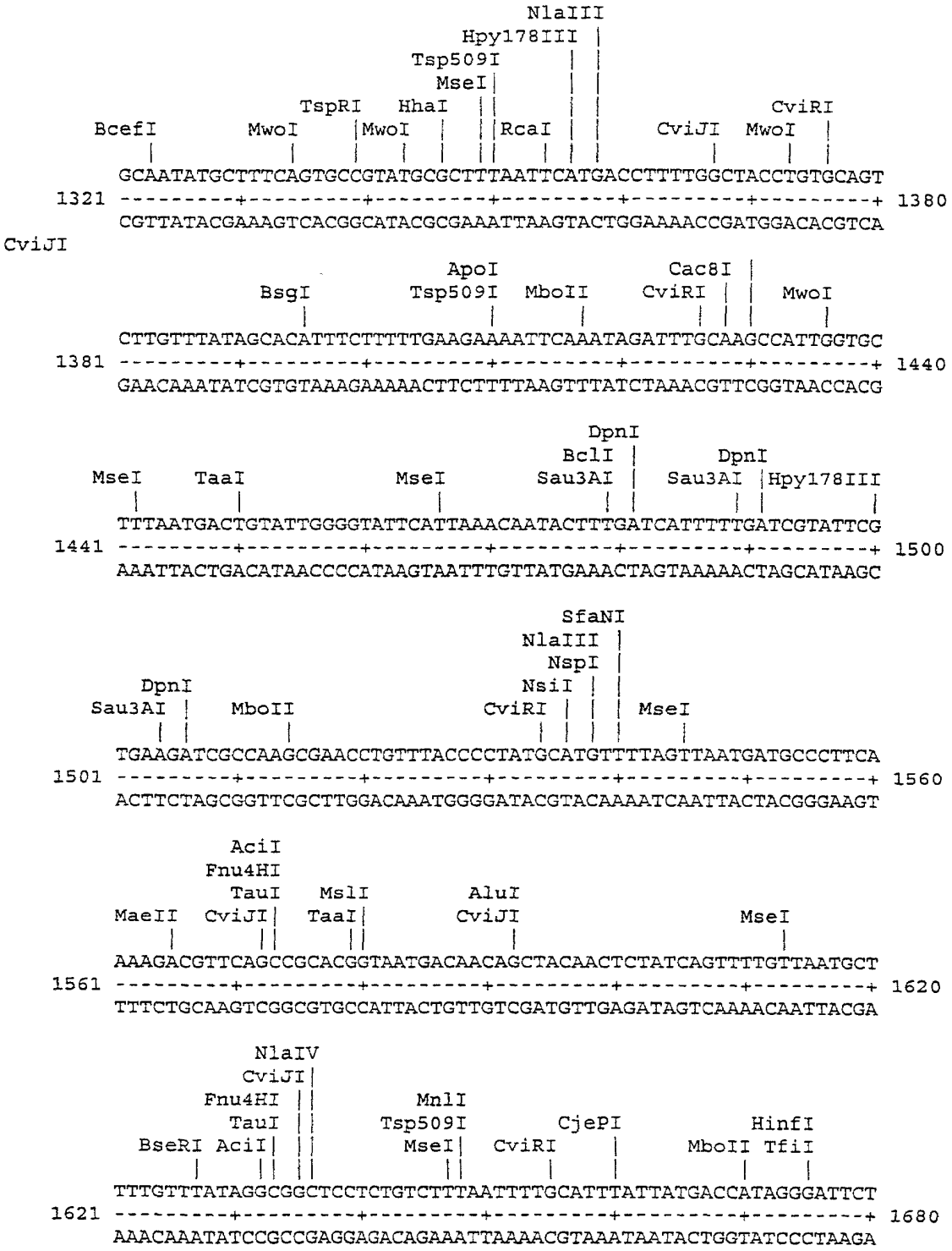


Figure 1 (continued)

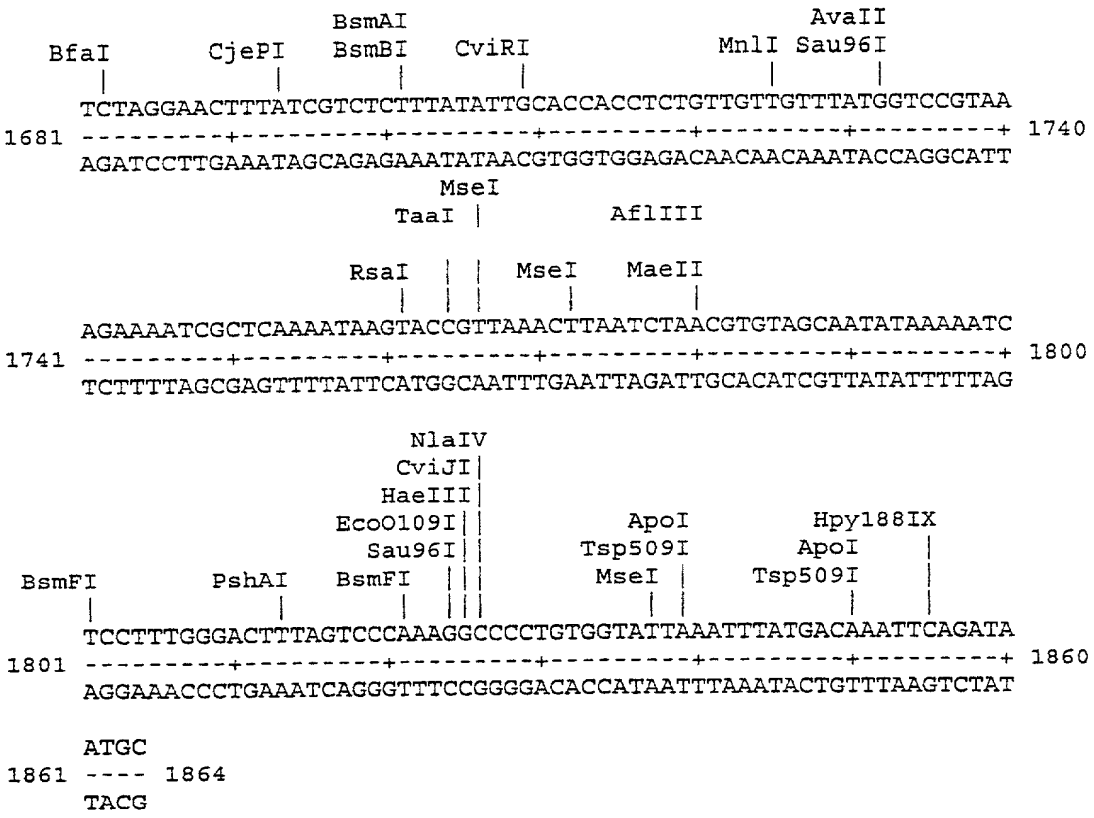
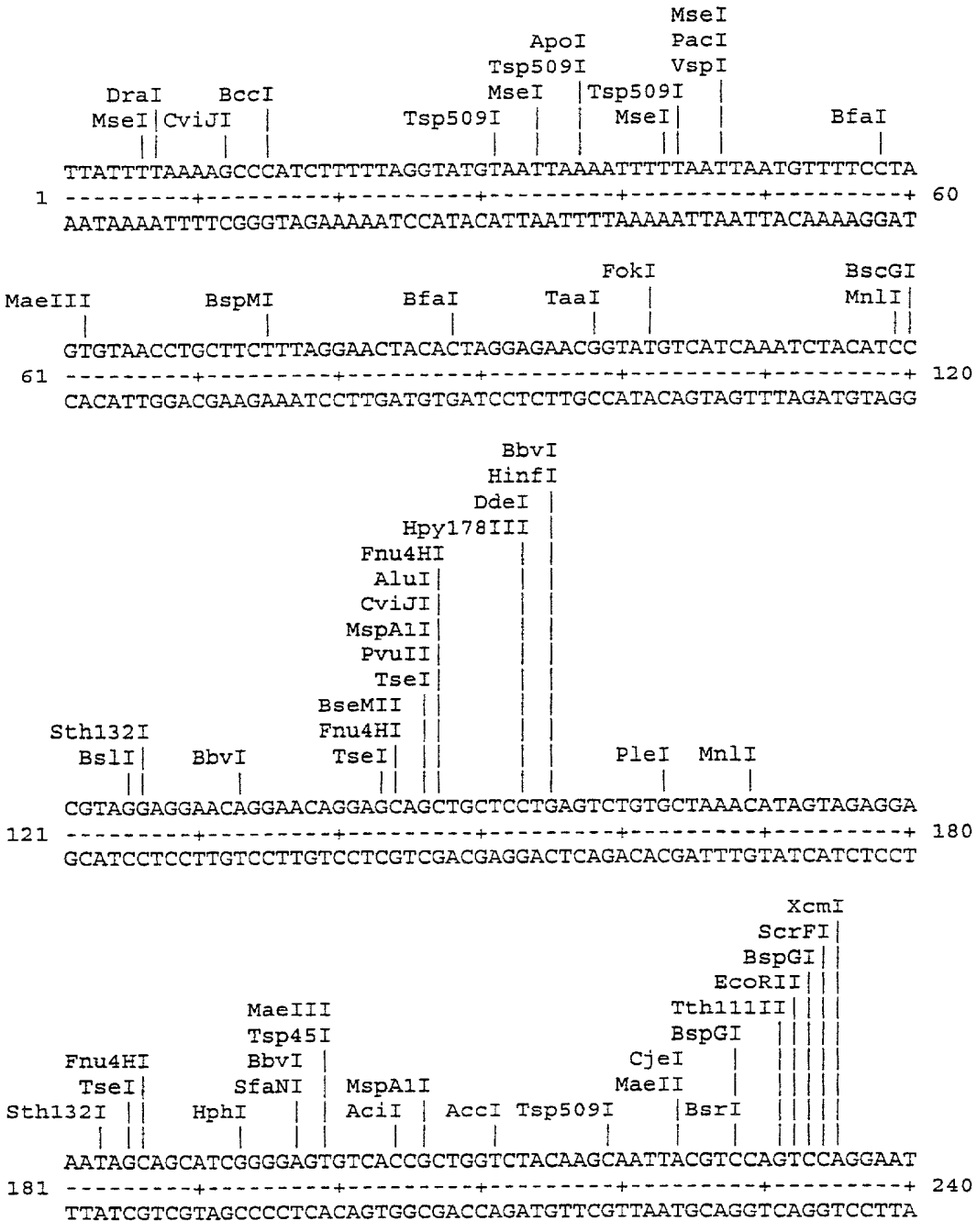


Figure 2

Restriction enzyme analysis of CPN100696 (RY 55 - SEQ ID NO. 2)



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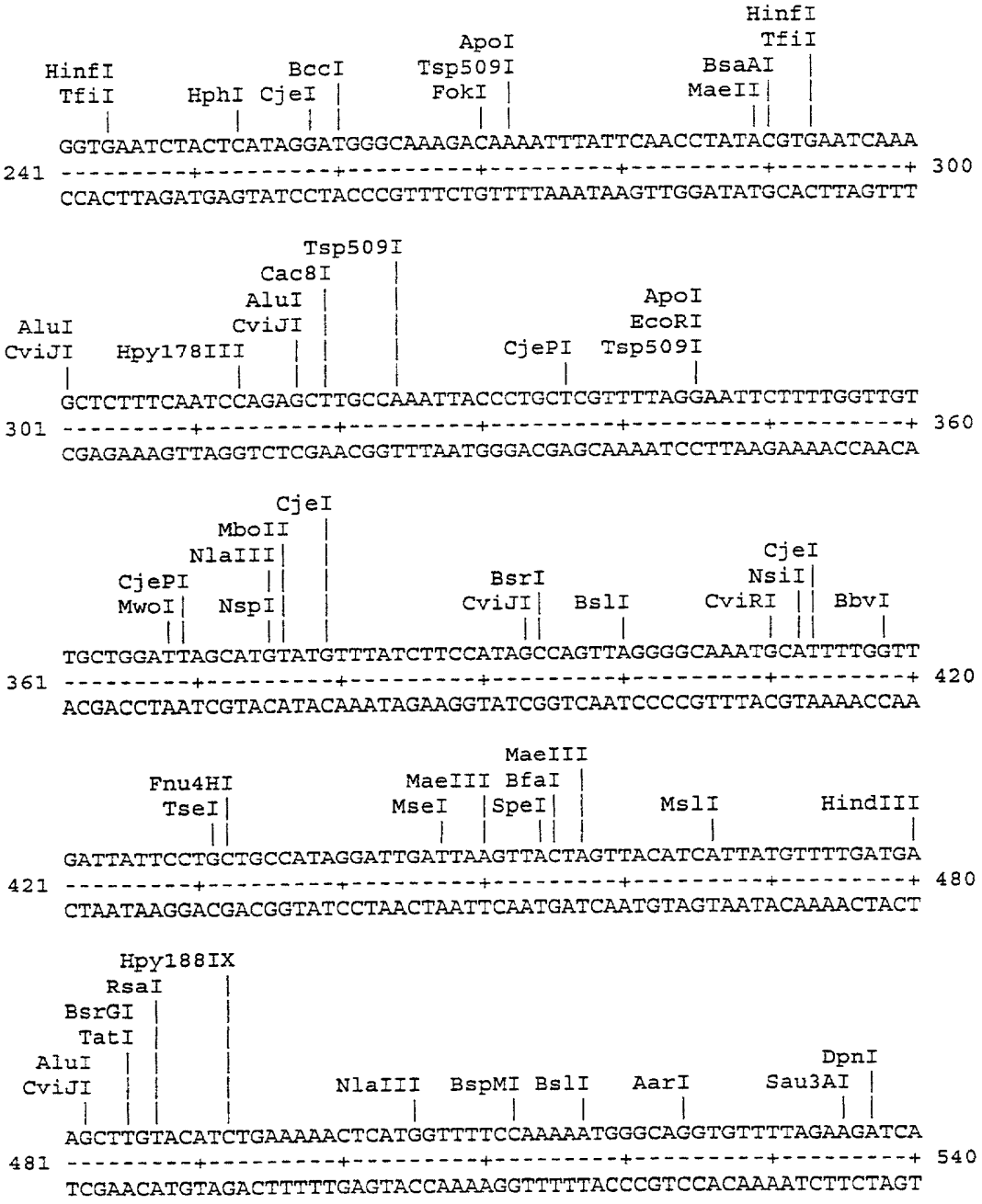

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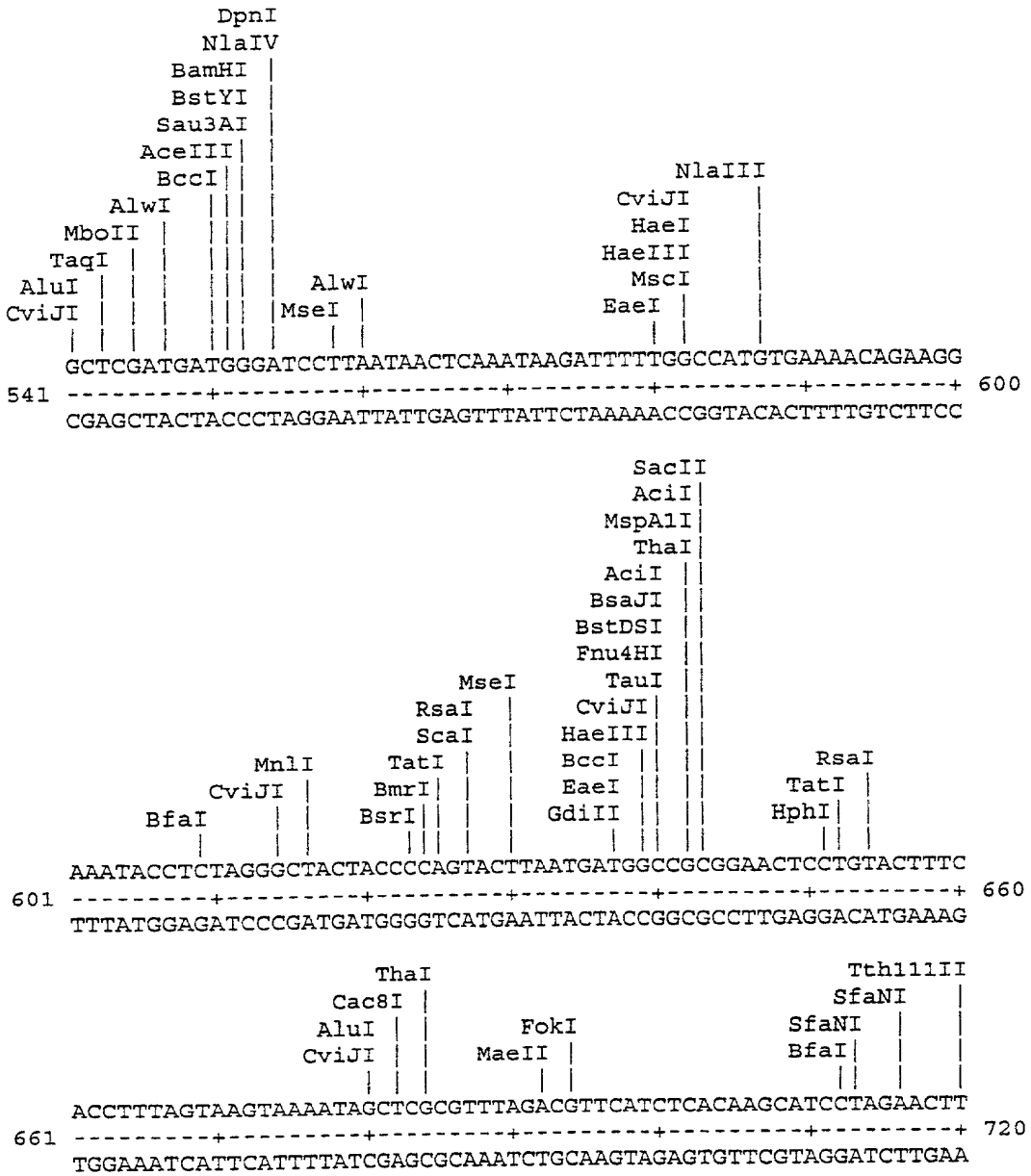


Figure 2 (continued)

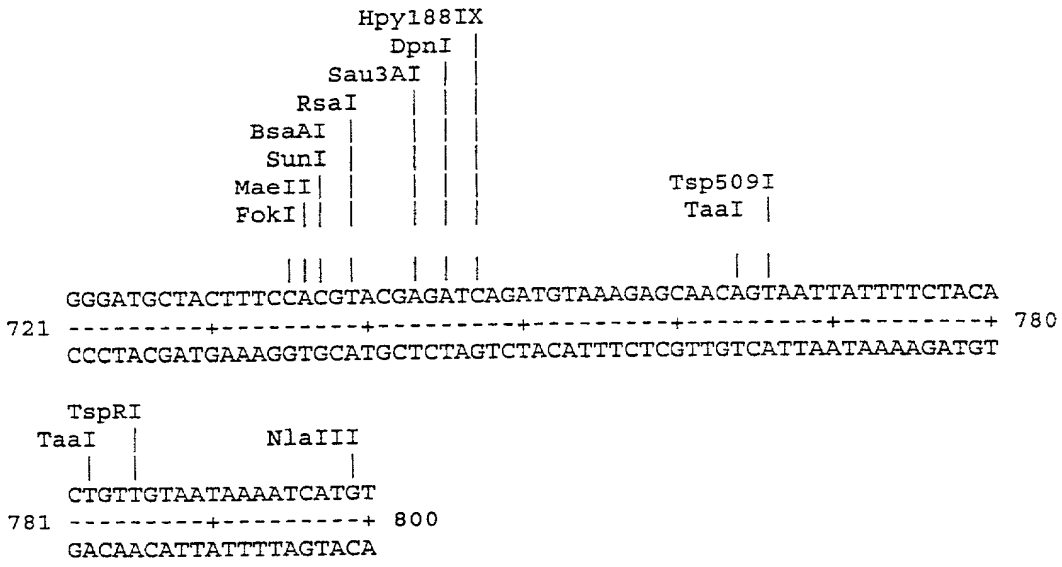
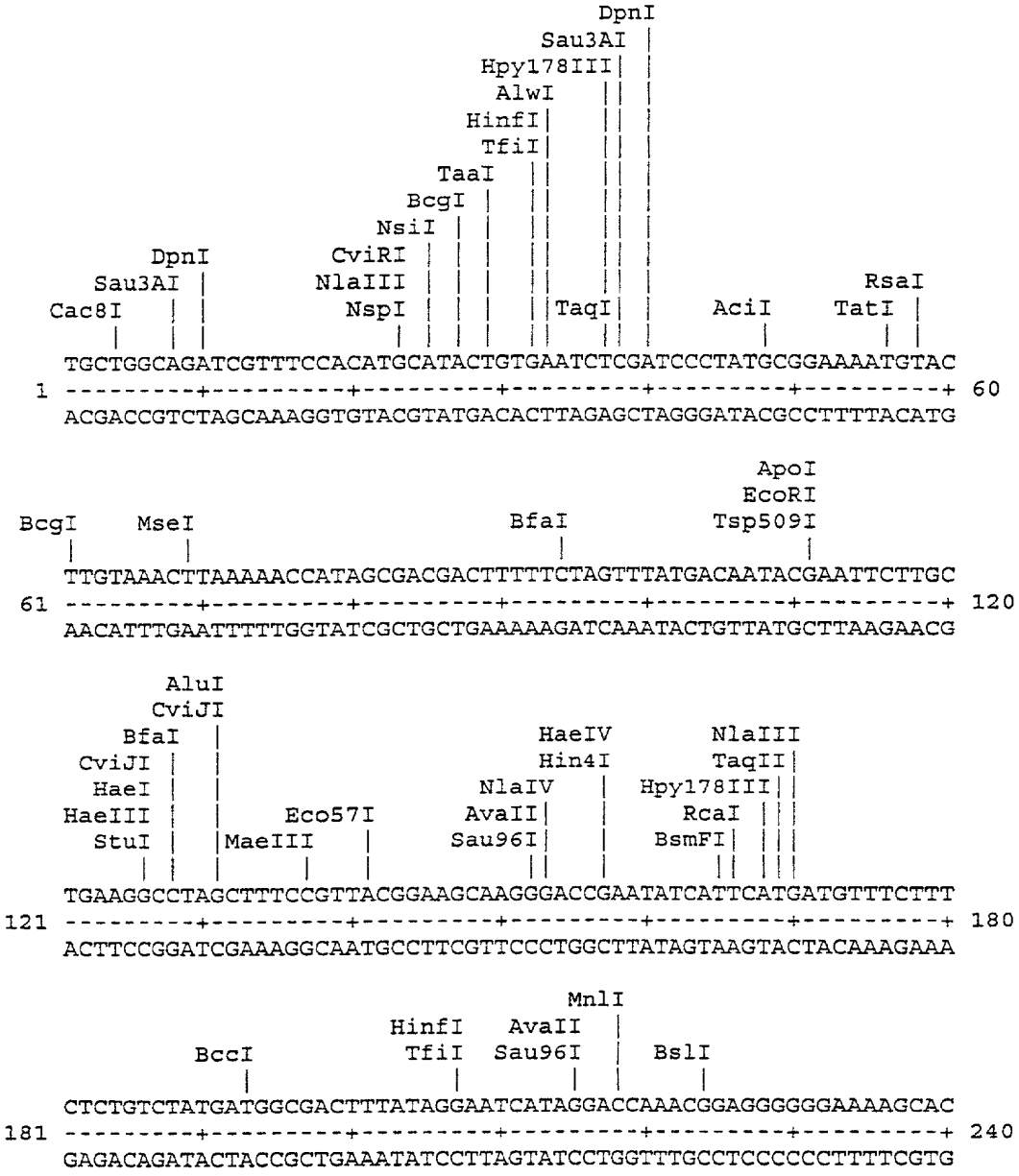


Figure 3
Restriction enzyme analysis of CPN100709 (RY 57 - SEQ ID NO. 3)



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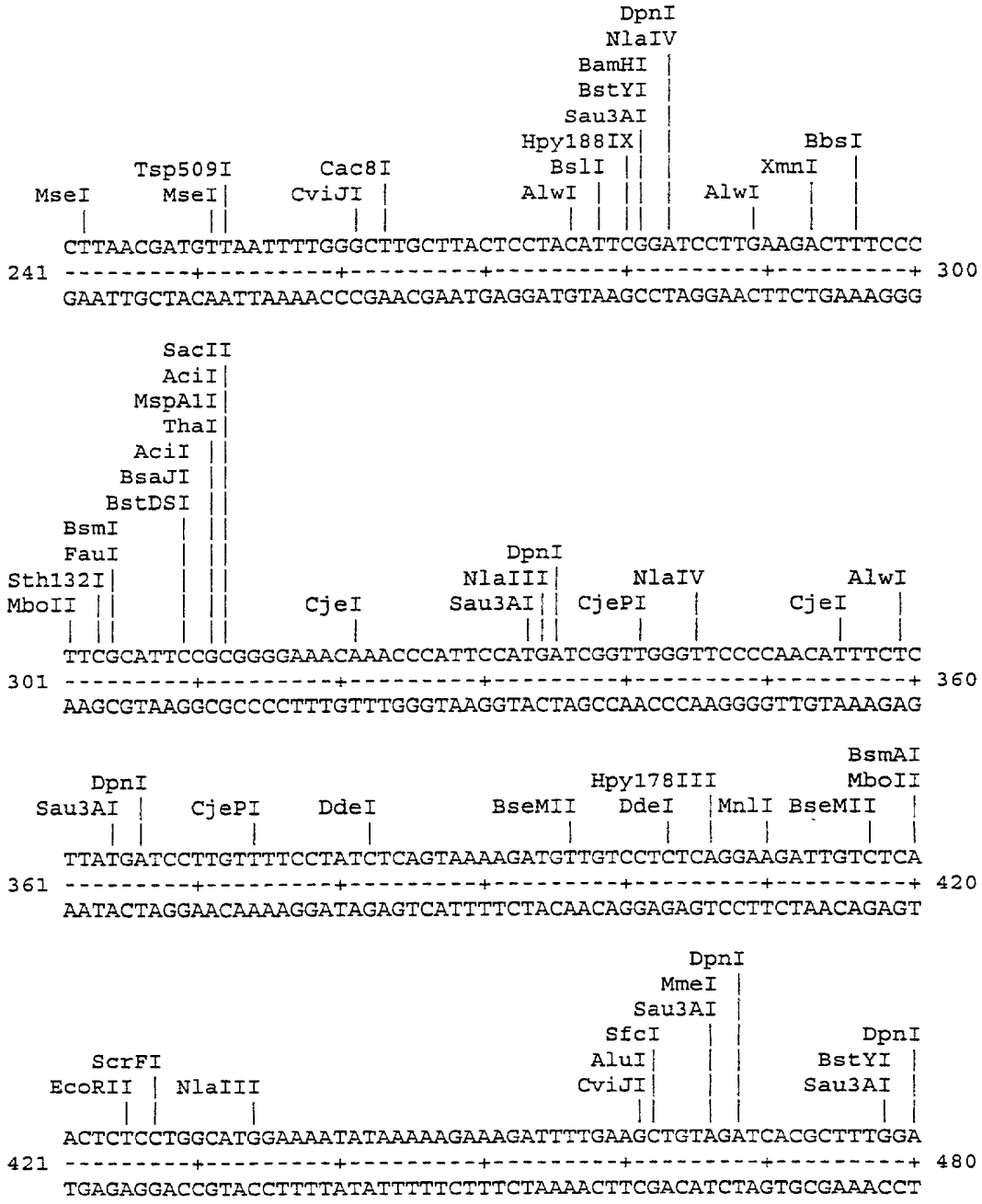

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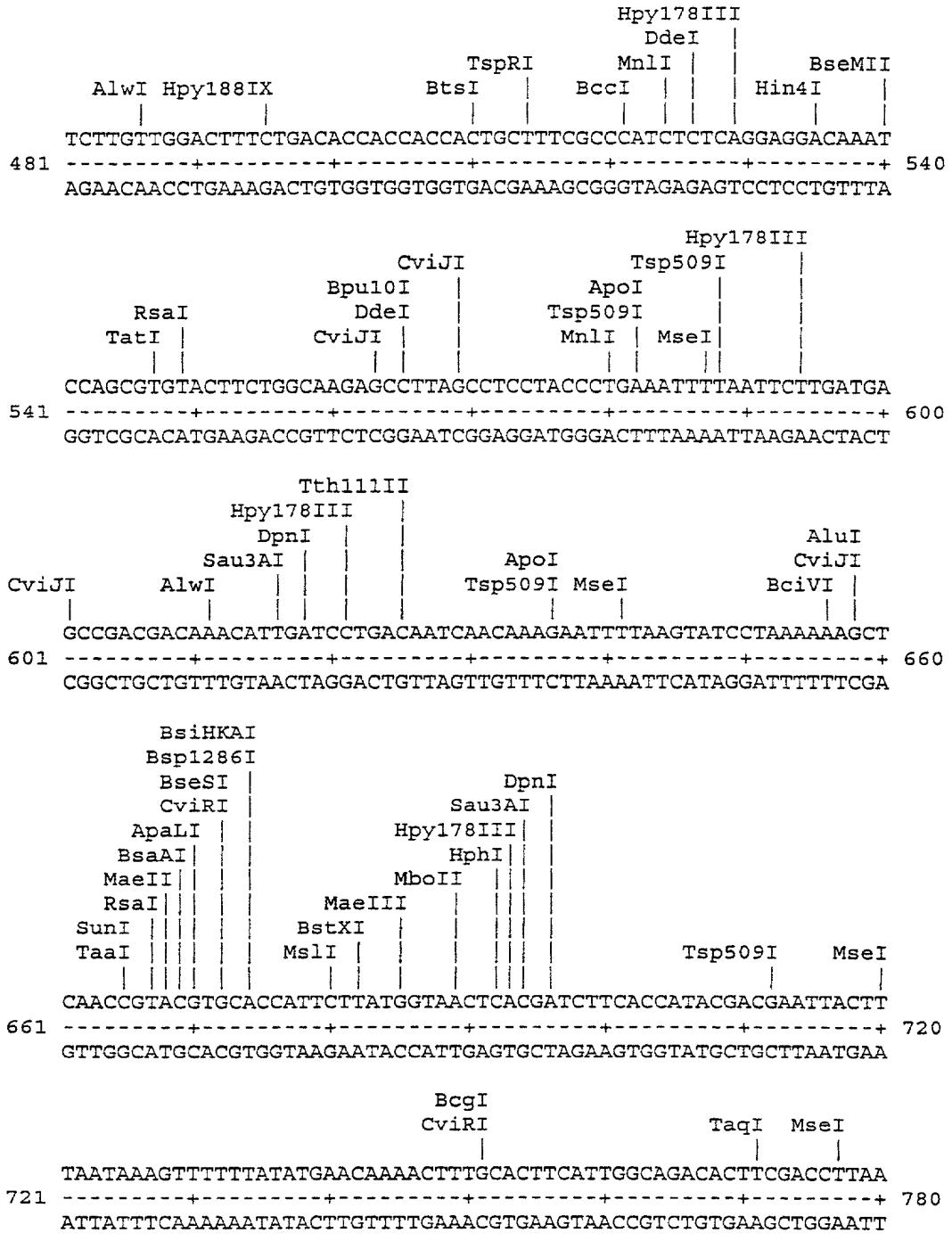

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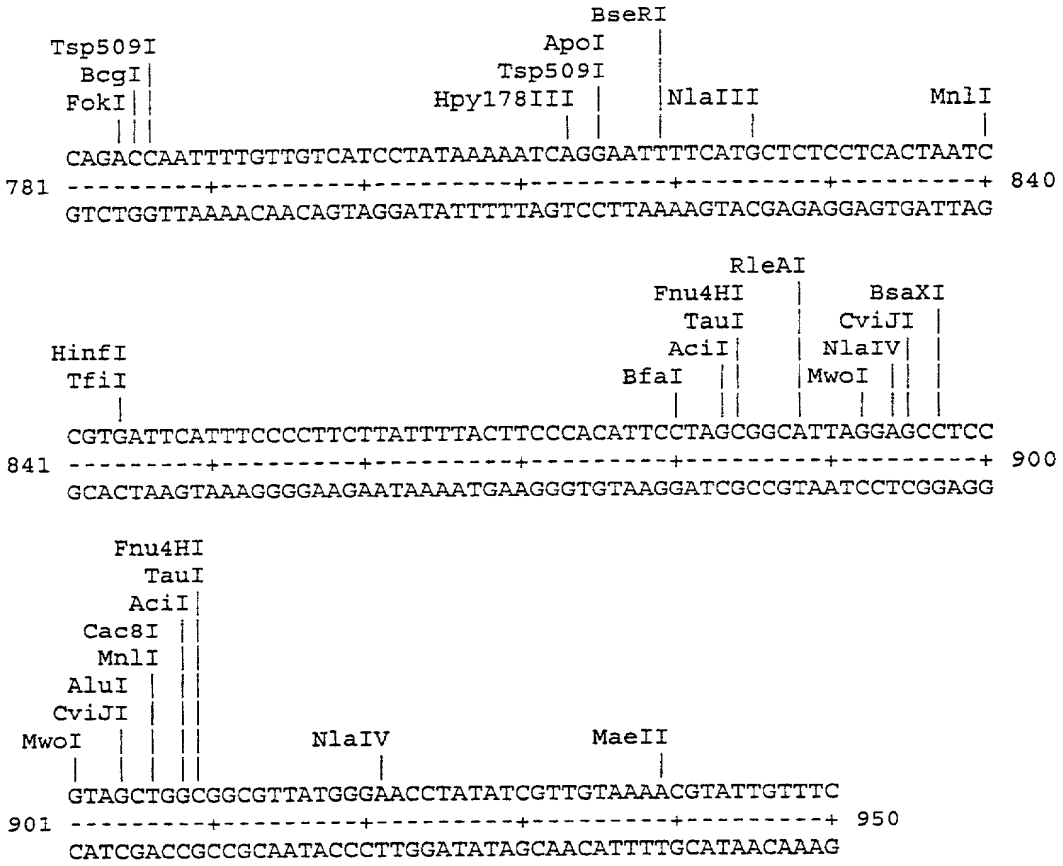

Figure 4
Restriction enzyme analysis of CPN100710 (RY 58 - SEQ ID NO. 4)

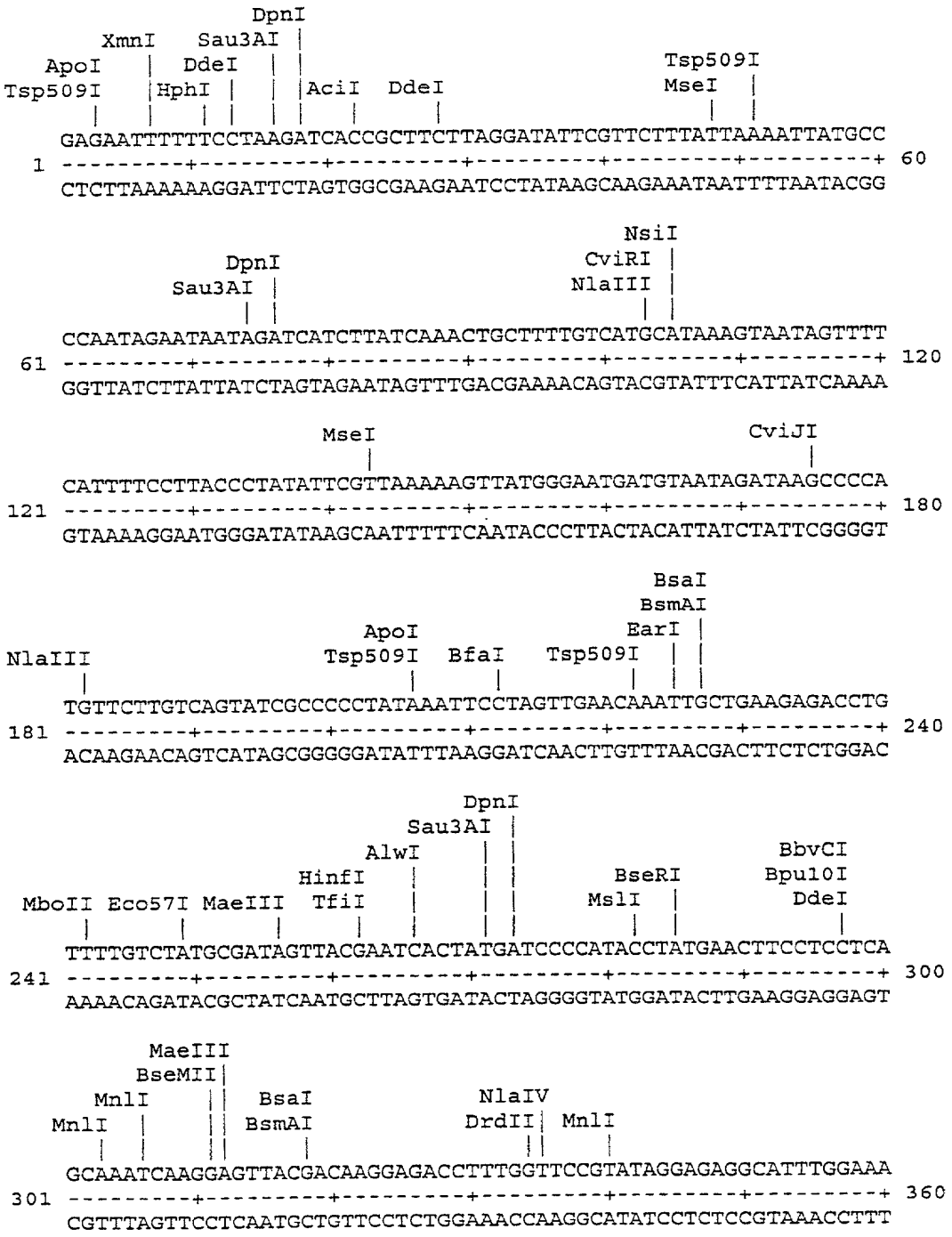

Figure 4 (continued)

```
                                         DpnI
                               CviRI   CjePI|                        HinfI
                              NlaIII  Sau3AI||                        TfiI
                                NspI   TaqI|||                  BsmAI   |
                                   |       ||||                     |   |
      AAACTTGTTAGAGAAACCTTACATGCAACAAGTCGATCTTTCCCAAAATGTCTCGCTGAT
  361 ---------+---------+---------+---------+---------+---------+ 420
      TTTGAACAATCTCTTTGGAATGTACGTTGTTCAGCTAGAAAGGGTTTTACAGAGCGACTA

                                                                 CviJI
          CviJI                          Pfl1108I                TaqII|
       CjePI |                             CjeI |         BslI MseI  ||
             | |                              | |            |    |  ||
      TCAAGGAAAGCCTTGCTGTAATCAACATACCACGAACTACGACACCCACACTTGGTTAAG
  421 ---------+---------+---------+---------+---------+---------+ 480
      AGTTCCTTTCGGAACGACATTAGTTGTATGGTGCTTGATGCTGTGGGTGTGAACCAATTC

                MseI                  MaeIII
   RleAI       CjeI|   BsmAI        CjeI  |          MseI
      |            ||      |           |   |            |
      CCCTAAAAACCTTAAAGTCCAAGTGGAGACTATCGTTACCACTTTAAGTAAAAAATATCC
  481 ---------+---------+---------+---------+---------+---------+ 540
      GGGATTTTTGGAATTTCAGGTTCACCTCTGATAGCAATGGTGAAATTCATTTTTTATAGG

               HaeIV
               Hin4I
           HinfI   |
           MnlI|   |
          ThaI||   |                                  AvaII
      BsbI    |||   |                                 Sau96I
      CjeI    |||   |                              AluI  |
      PleI    |||   |             BsrDI           CviJI  |    MnlI
         |    |||   |                 |                 |    |     |
      TCAACACGCGACTCTATATCAAAGCAATGGAGAGAAACTTCTGTTAGCTTTGGACCAACT
  541 ---------+---------+---------+---------+---------+---------+ 600
      AGTTGTGCGCTGAGATATAGTTTCGTTACCTCTCTTTGAAGACAATCGAAACCTGGTTGA

                                                             BsaJI
                                                            BstDSI
           ApoI                                               NcoI
        Tsp509I                     MnlI                      StyI
              |                        |                         |
      CAATGAGGAAATTCTTACGATTACCTCCAAAGCGAAACAACGCCATATTTTAGTTTCCCA
  601 ---------+---------+---------+---------+---------+---------+ 660
      GTTACTCCTTTAAGAATGCTAATGGAGGTTTCGCTTTGTTGCGGTATAAAATCAAAGGGT
```

Figure 4 (continued)

```
              BcefI
            CviJI |
              XcmI |
           NlaIV|  |
        NlaIII ||  |         Tsp509I     DdeI      SfcI   BseMII
             | ||  |               |        |         |       |

    TGGAGCCTTTGGGTATTTTTGCCGTGATTACAATTTCTCTCAGCACACTATAGAGAAAAG
661 ---------+---------+---------+---------+---------+---------+ 720
    ACCTCGGAAACCCATAAAAACGGCACTAATGTTAAAGAGAGTCGTGTGATATCTCTTTTC

                                            Hpy178III      MboII
                                         ThaI       |      RsaI|
                  CviJI              Cac8I |  MaeIII|      TaaI ||
          NlaIII      |           CviJI |  |  Tsp45I|      TatI ||
               |      |               | |  |      ||           | ||
    CAGTCATGTTGAGCCTTCTCCTAAAGATGTGGCTCGCGTATTTCGTGACATTGAACAGTA
721 ---------+---------+---------+---------+---------+---------+ 780
    GTCAGTACAACTCGGAAGAGGATTTCTACACCGAGCGCATAAAGCACTGTAACTTGTCAT

                          Hpy178III
    ApoI             HinfI      |                       MboII    Cac8I
Tsp509I       MboII TfiI     TaqI Hpy178III        BbsI     |    MwoI|
      |           |    |        |         |          |     |       ||
    CAAAATTTCTTCTGTGATTCTTCTCGAATACTCTGGAAGACGAAGTAGTGCTATGCTGGC
781 ---------+---------+---------+---------+---------+---------+ 840
    GTTTTAAAGAAGACACTAAGAAGAGCTTATGAGACCTTCTGCTTCATCACGATACGACCG

                                         DpnI
                                    Sau3AI |
                                Hpy178III| |
                                     AlwI || |
                                   HinfI| || |
                                    TfiI| || |
                              TaaI   || || |
                           BcgI  |   || || |
                        NsiI  |  |   || || |
                    CviRI  |  |  |   || || |
    DpnI           NlaIII  |  |  |   || || |                     BcgI
Sau3AI |             NspI  |  |  |   ||TaqI| |       AciI    RsaI  |
     | |                |  |  |  |   ||    || |          |  TatI |  |
                                                               |  |  |
    AGATCGTTTCCACATGCATACTGTGAATCTCGATCCCTATGCGGAAAATGTACTTGTAAA
841 ---------+---------+---------+---------+---------+---------+ 900
    TCTAGCAAAGGTGTACGTATGACACTTAGAGCTAGGGATACGCCTTTTACATGAACATTT

                                                               CviJI
                                                  ApoI          HaeI
                                                 EcoRI        HaeIII
   MseI                        BfaI            Tsp509I          StuI
      |                           |                  |             |
    CTTAAAAACCATAGCGACGACTTTTTCTAGTTTATGACAATACGAATTCTTGCTGAAGGC
901 ---------+---------+---------+---------+---------+---------+ 960
    GAATTTTTGGTATCGCTGCTGAAAAAGATCAAATACTGTTATGCTTAAGAACGACTTCCG
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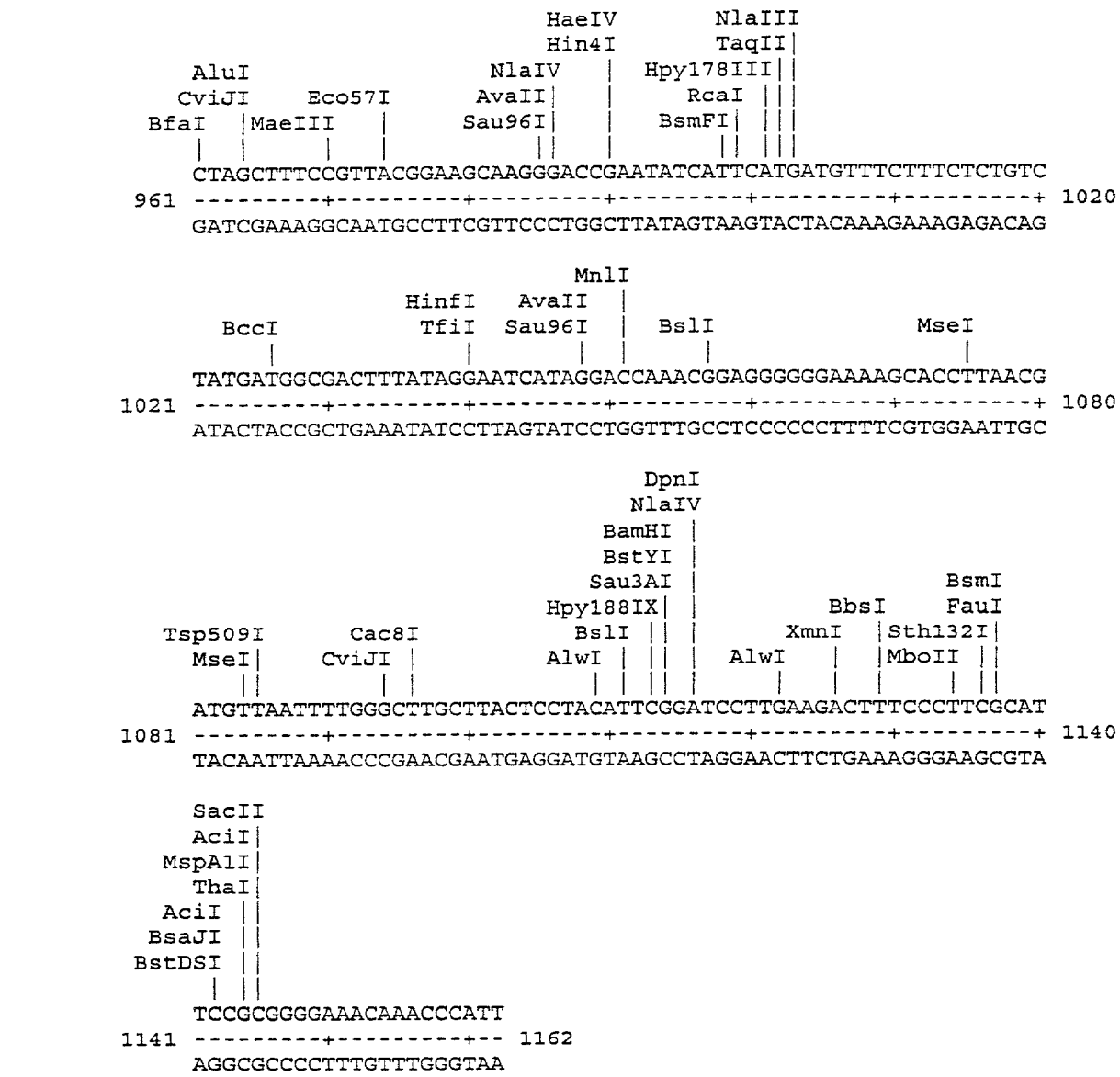
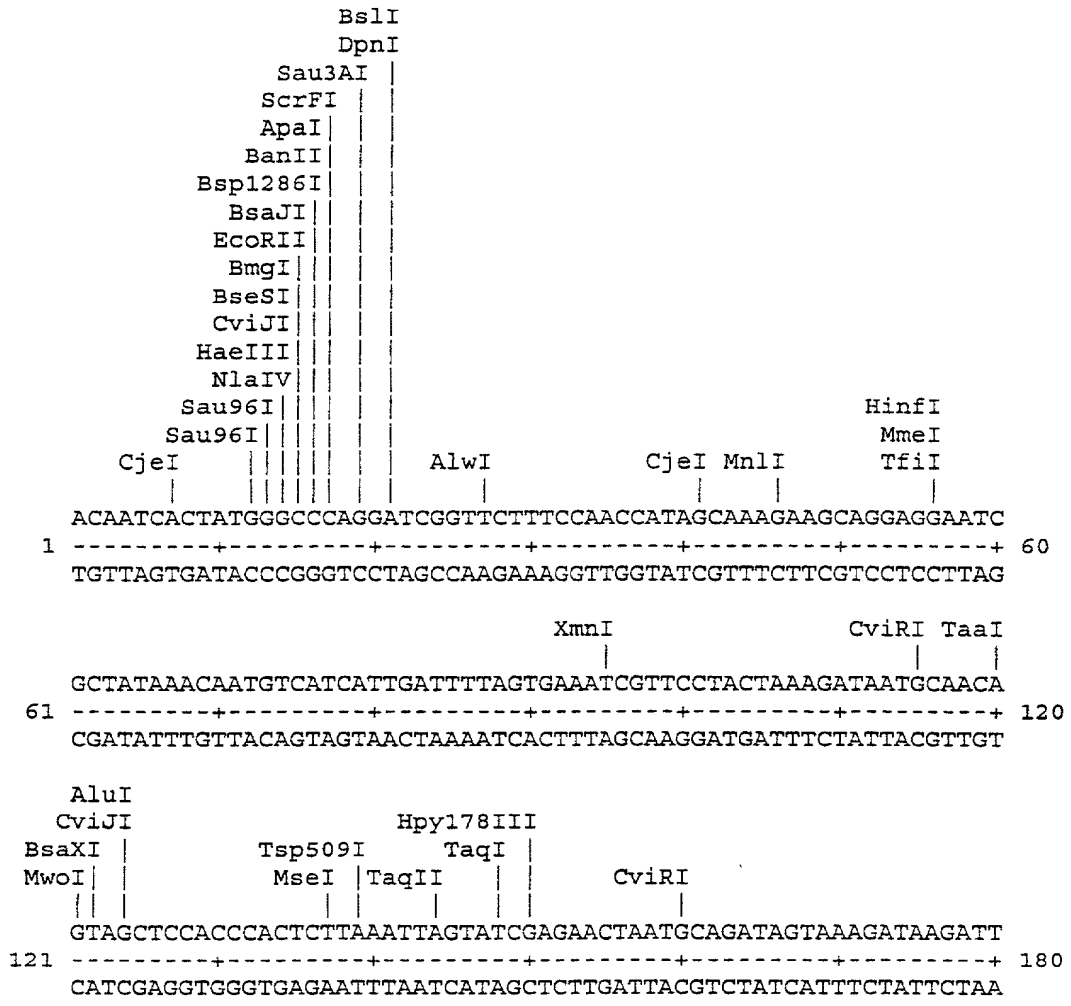


Figure 5

Restriction enzyme analysis of CPN100711 (RY 59 - SEQ ID NO. 5)



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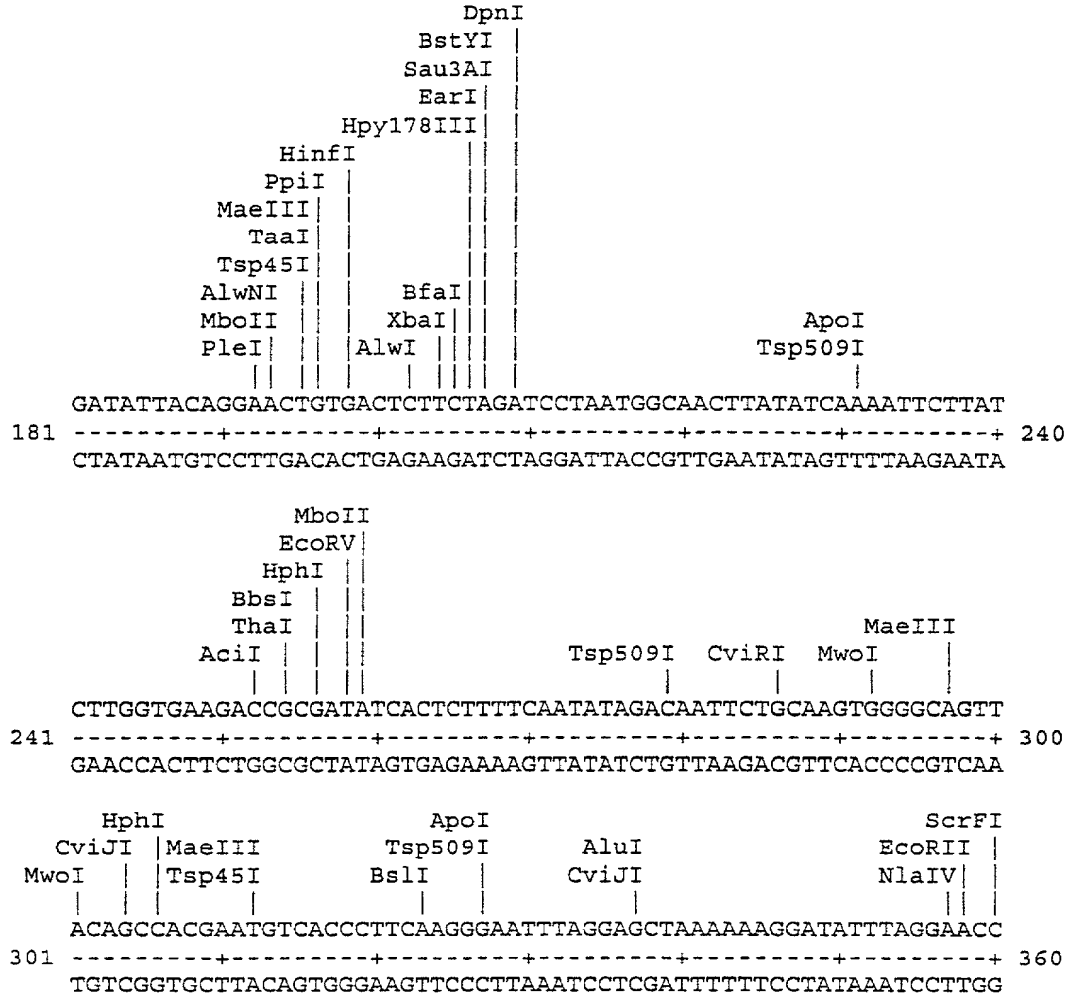

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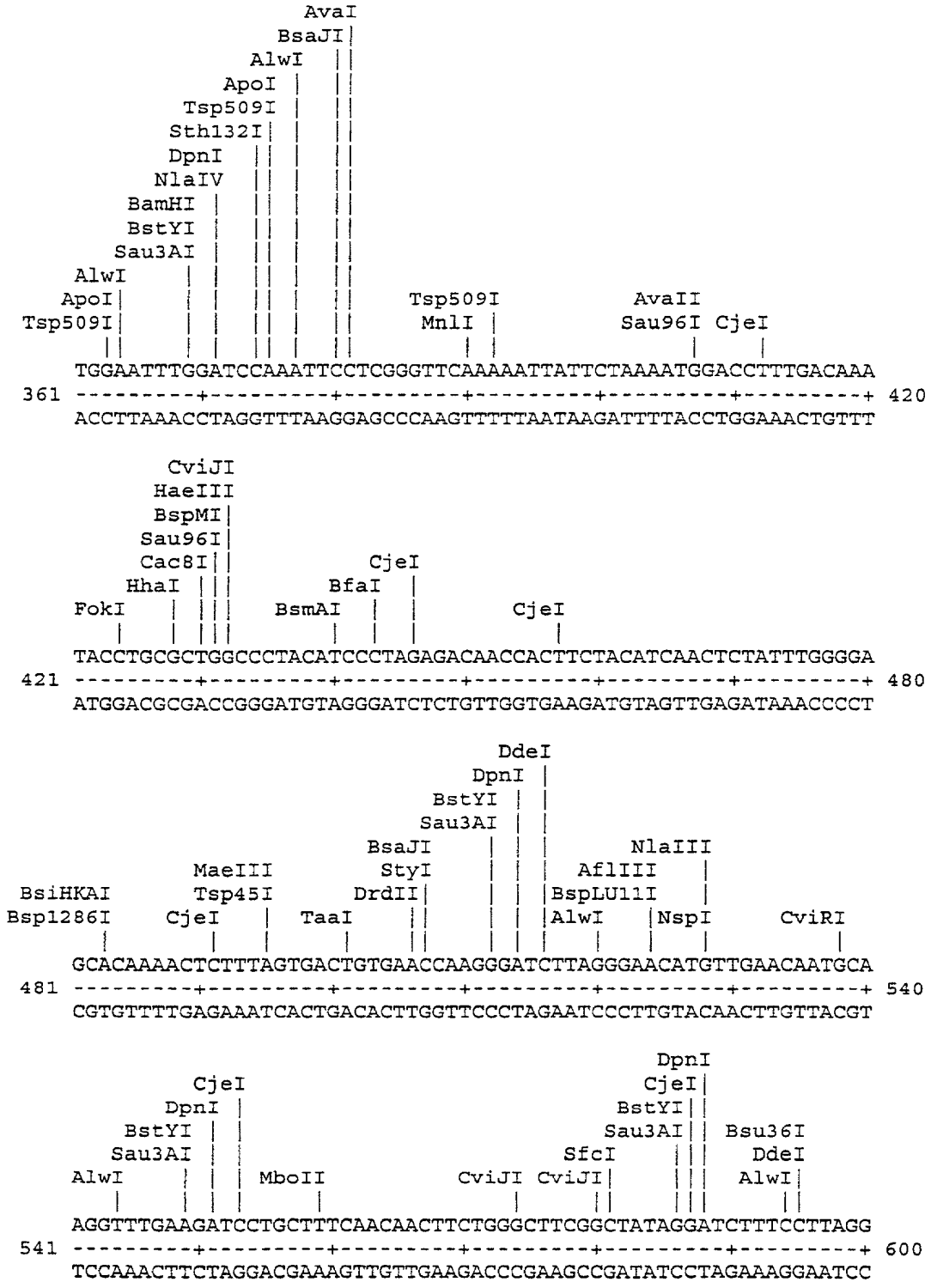

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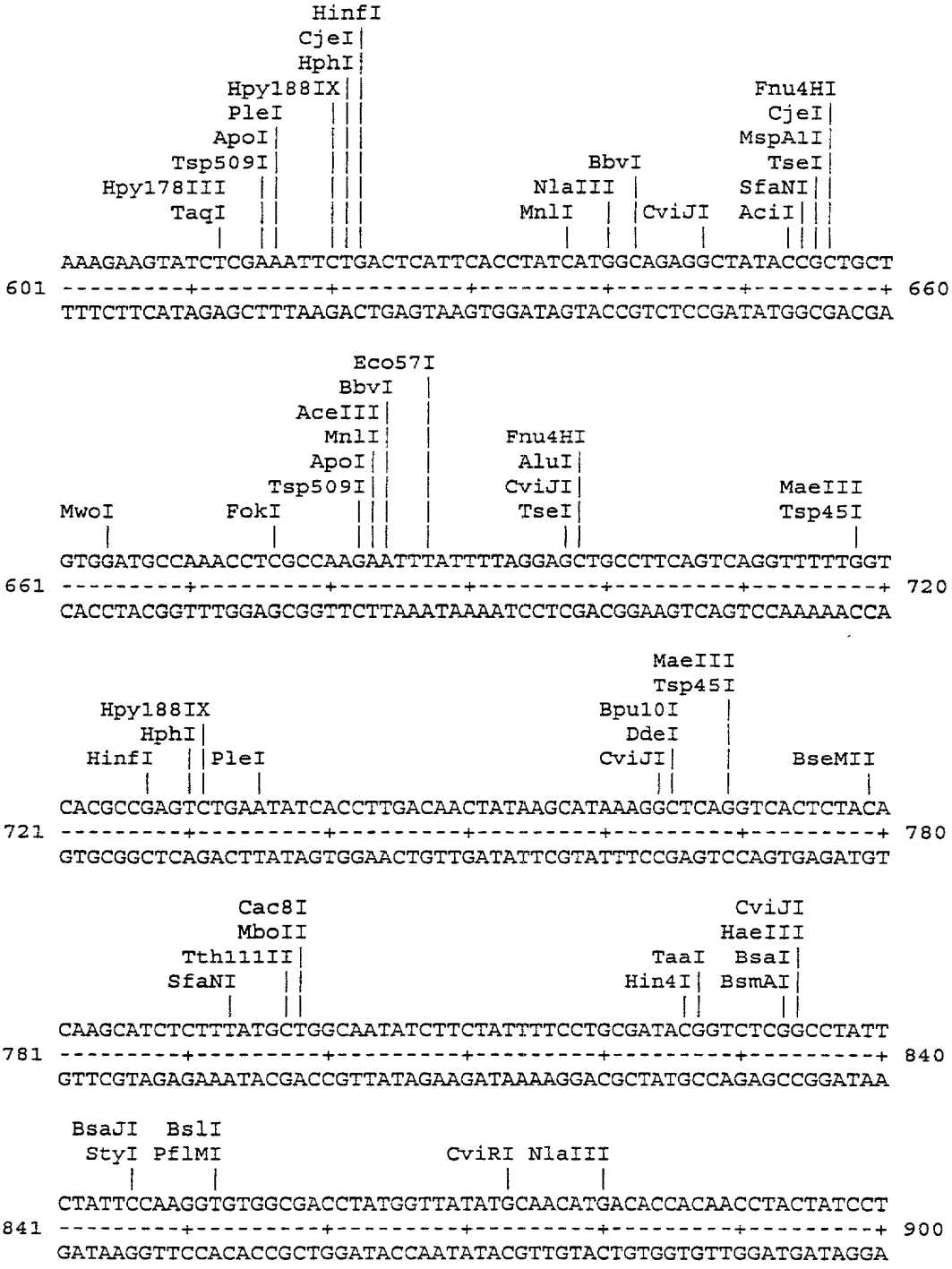

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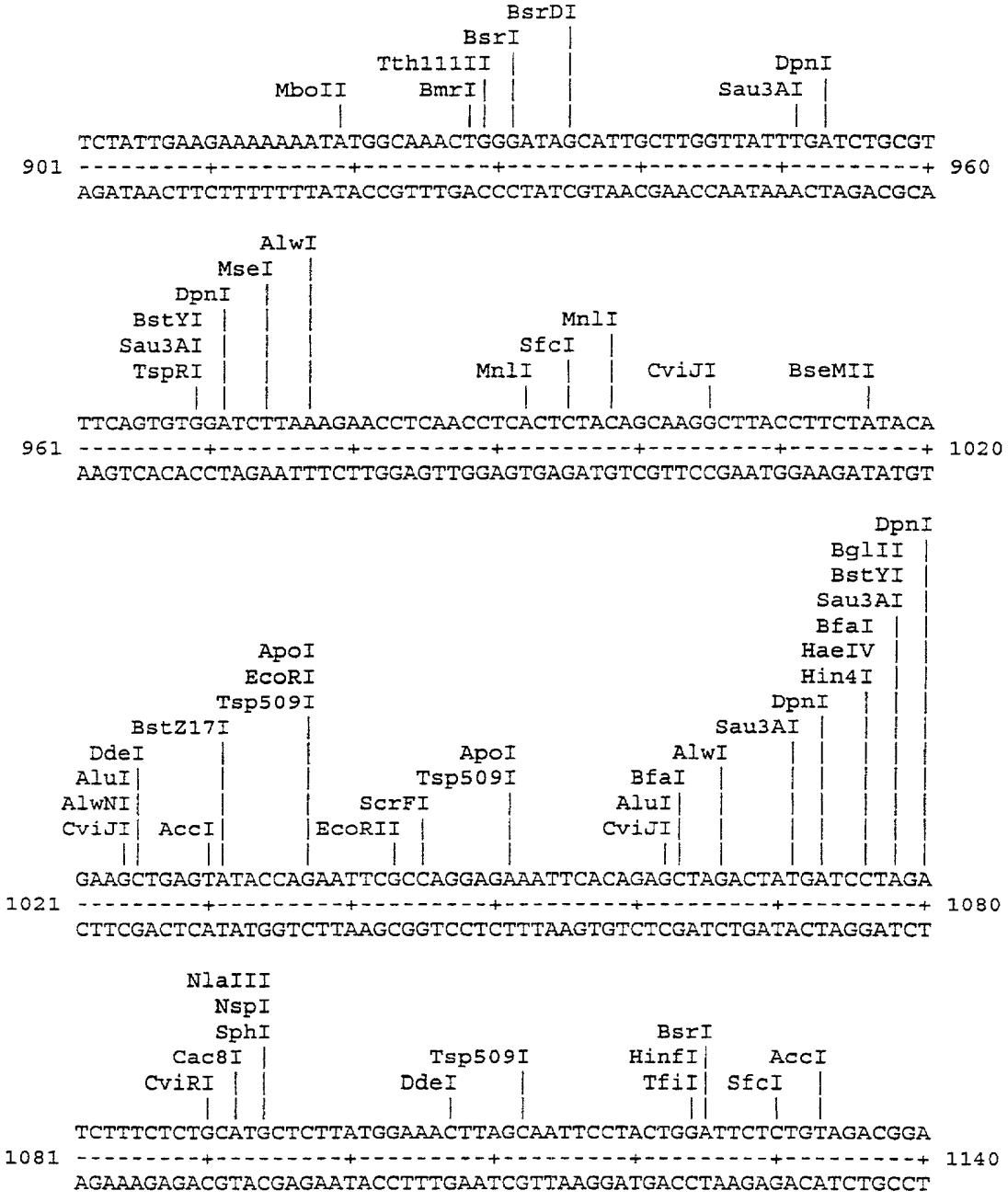

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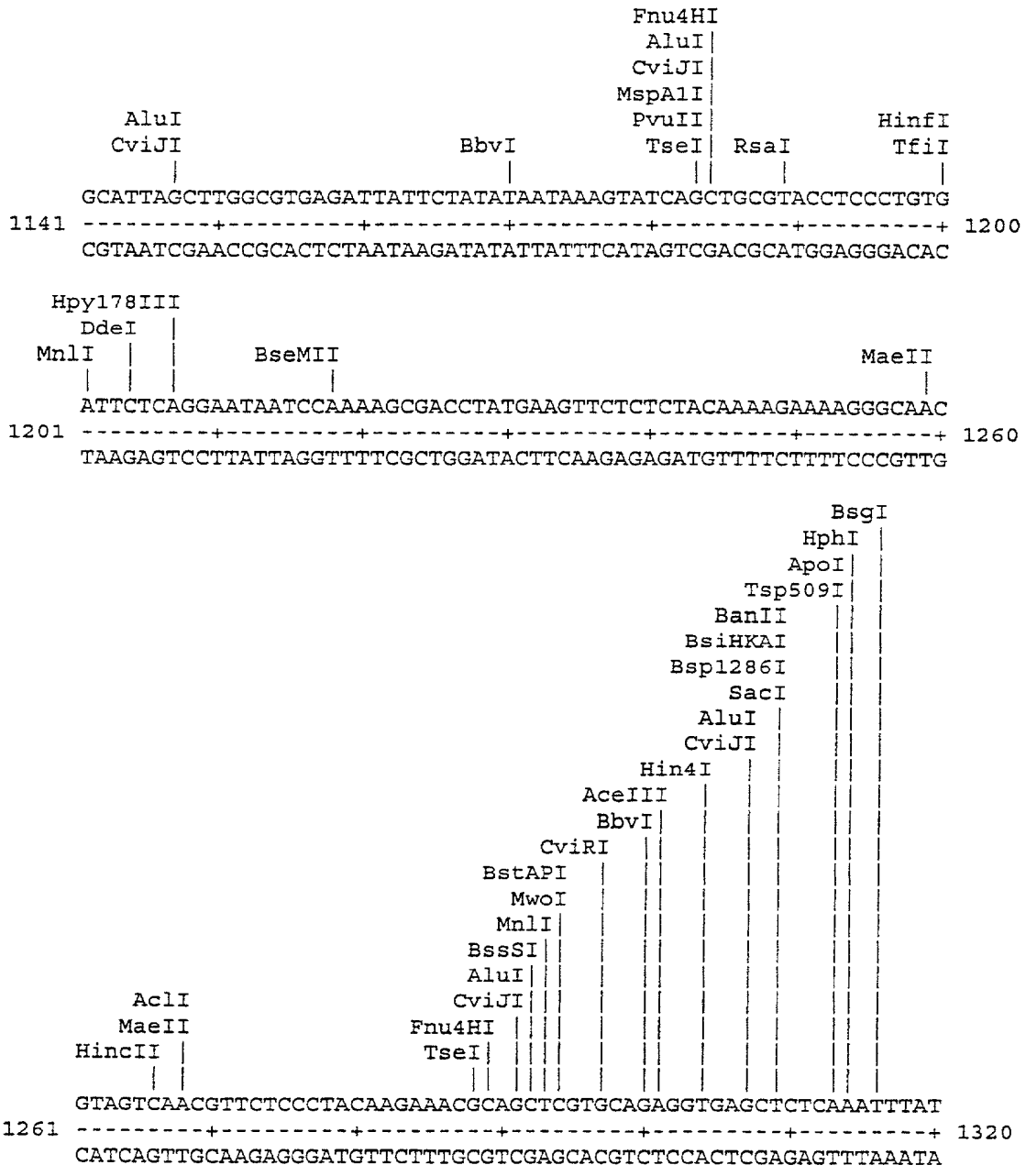

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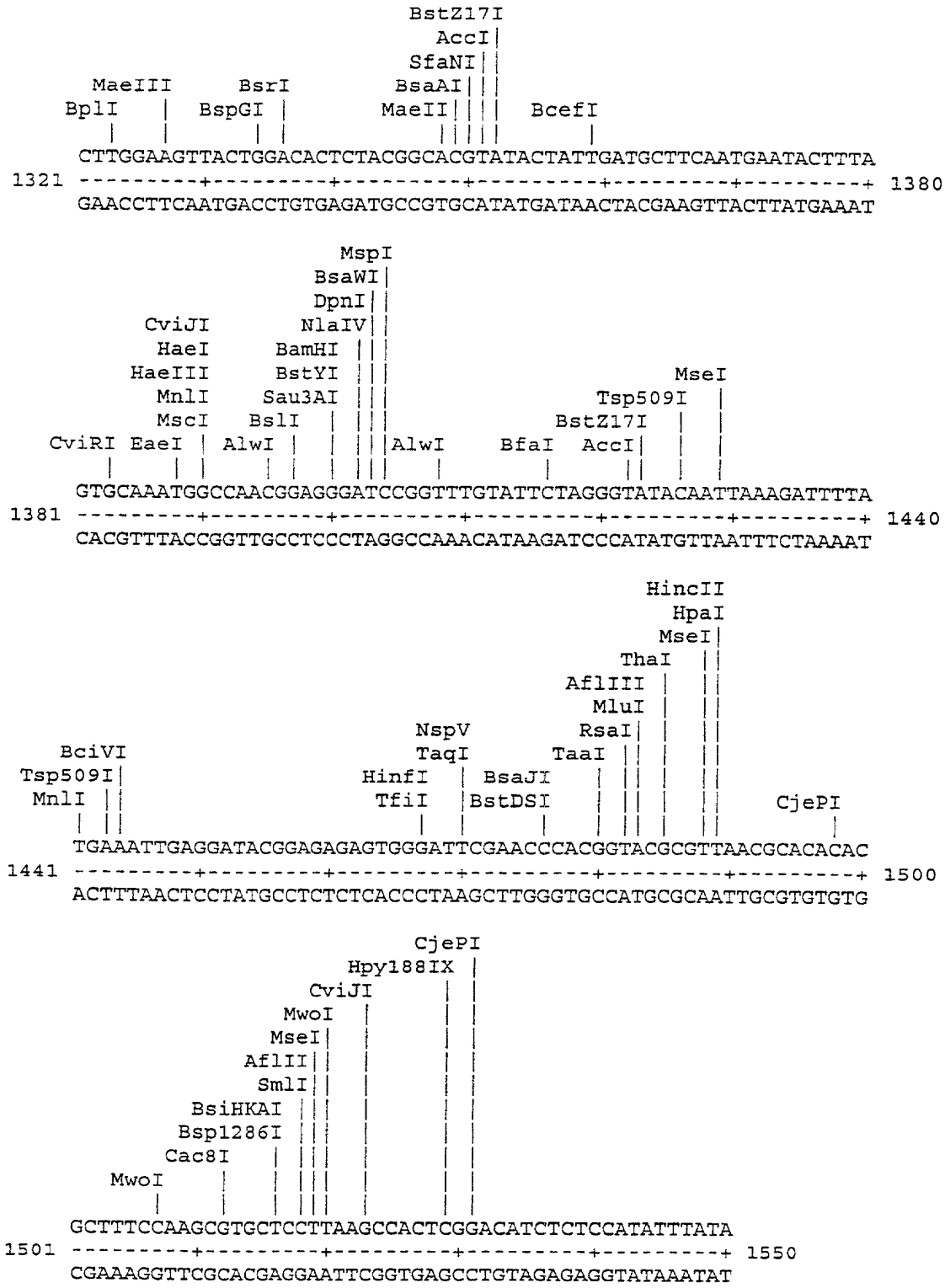
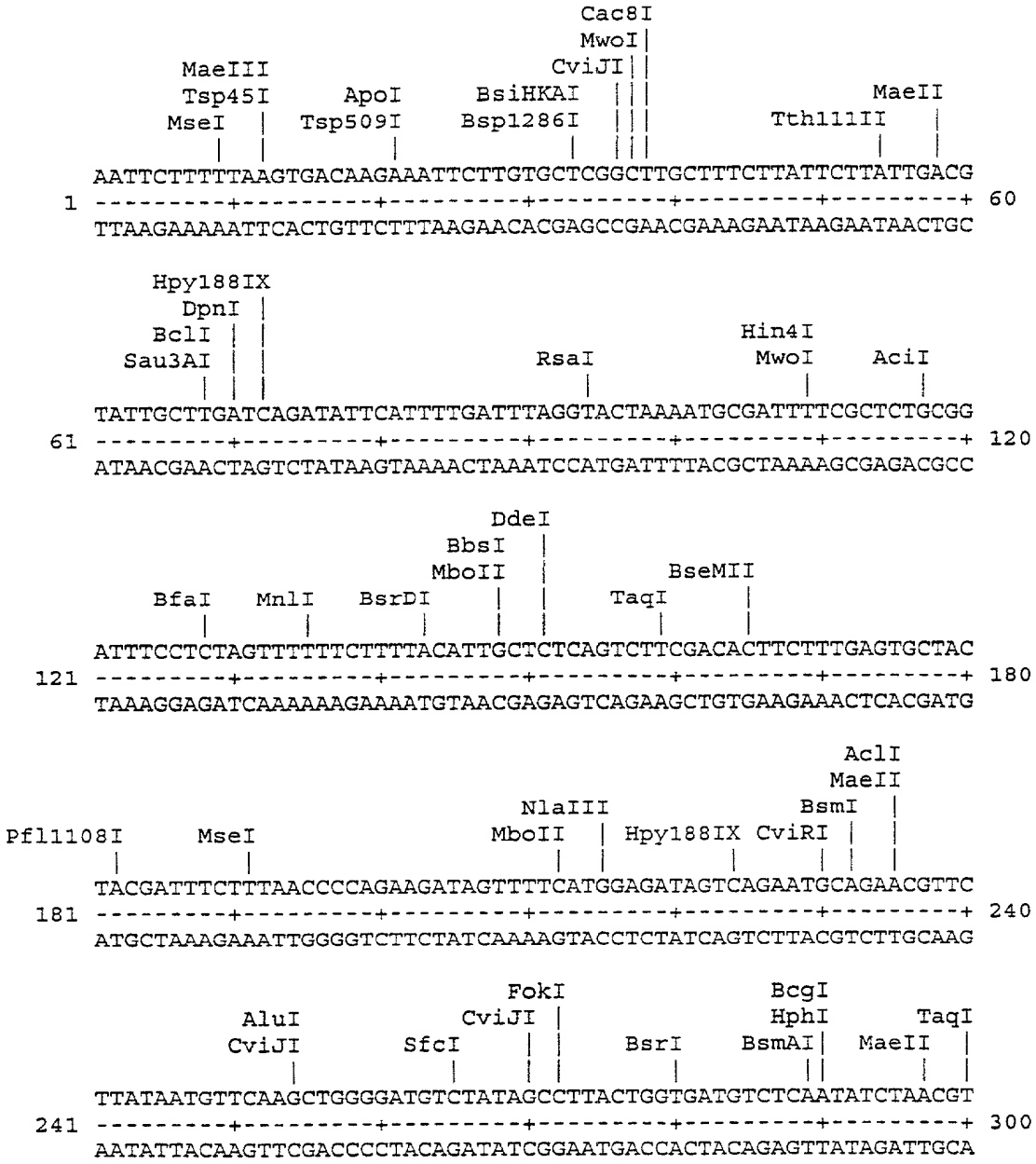


Figure 6

Restriction enzyme analysis of CPN100877 (RY 61 - SEQ ID NO. 6)



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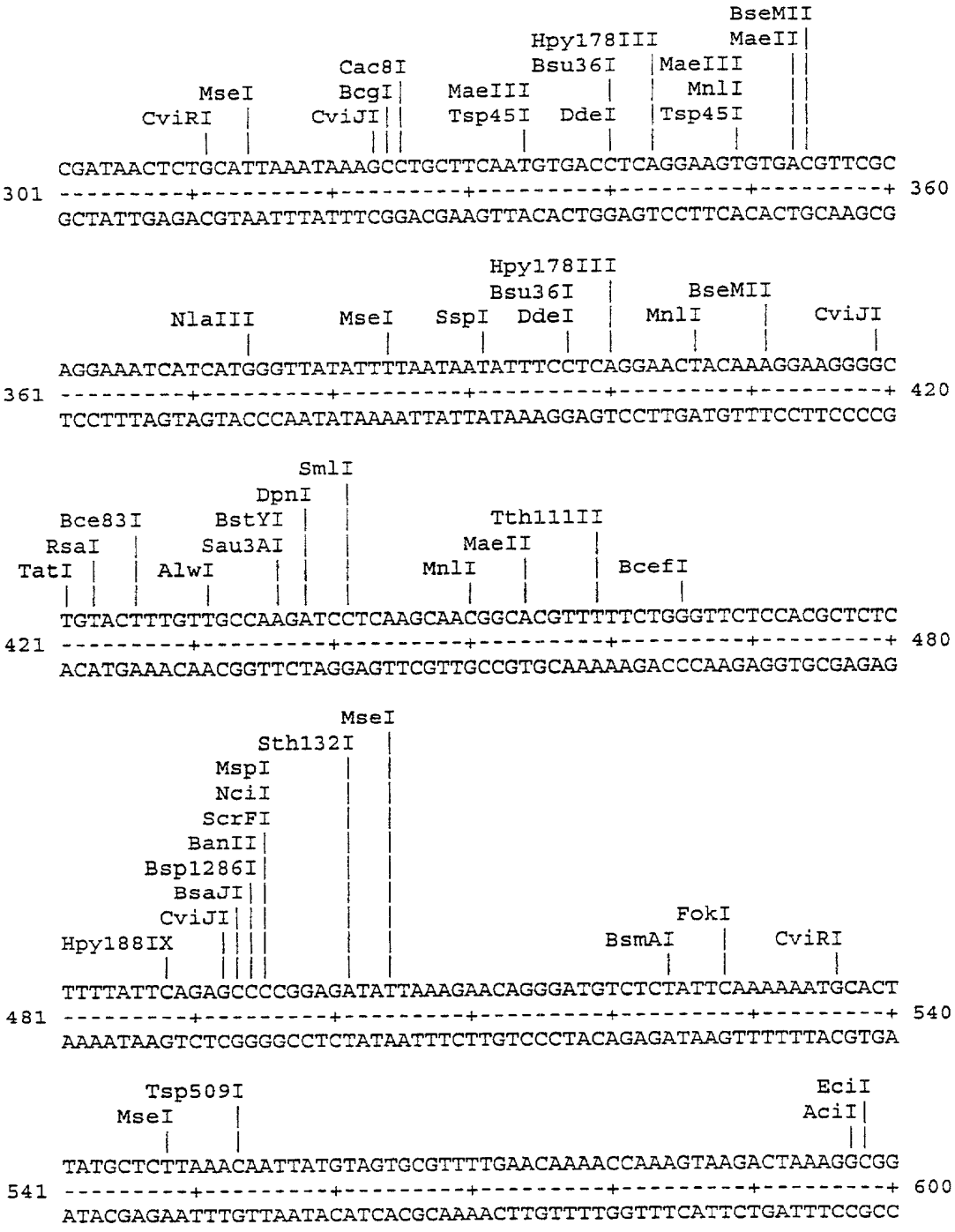

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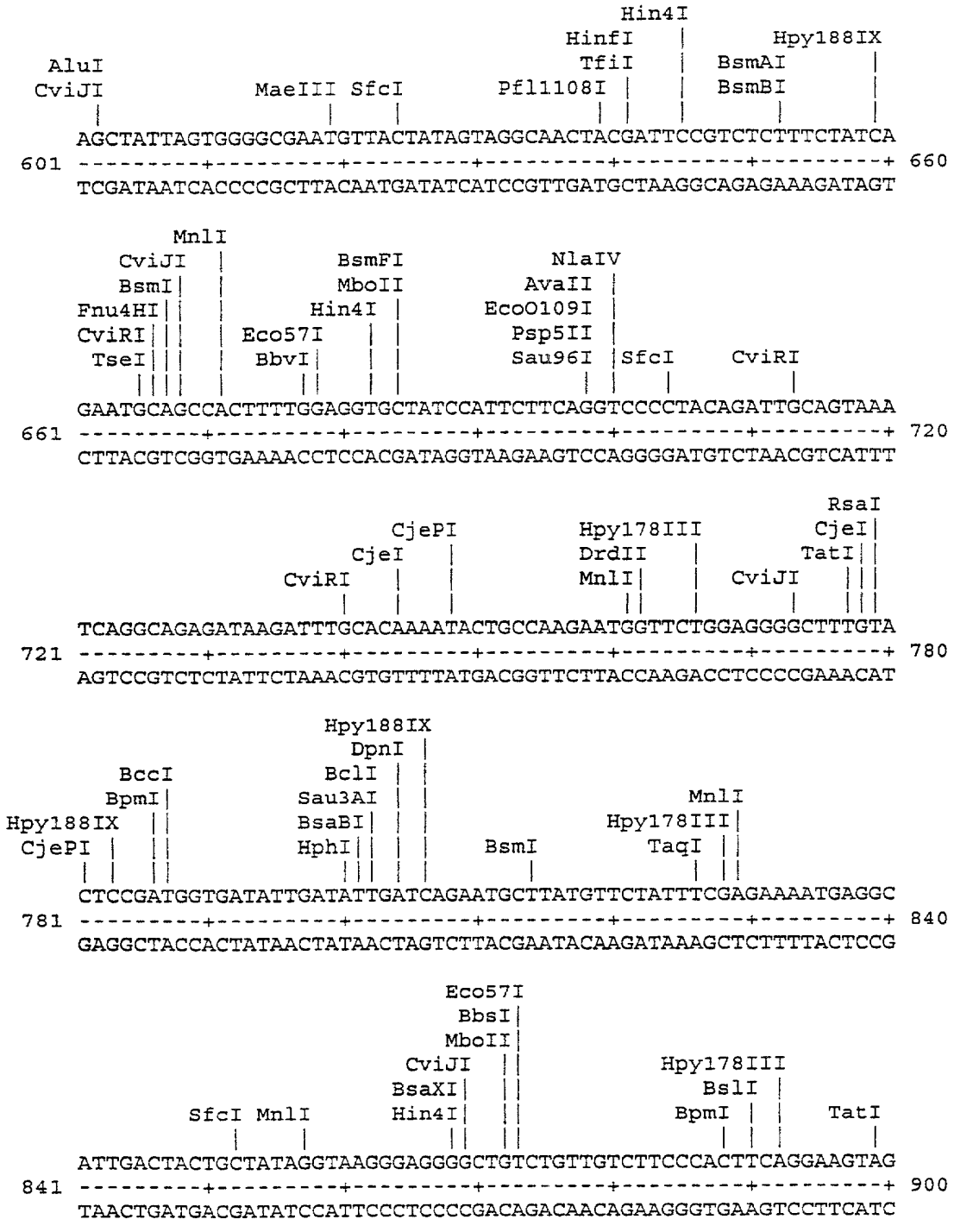

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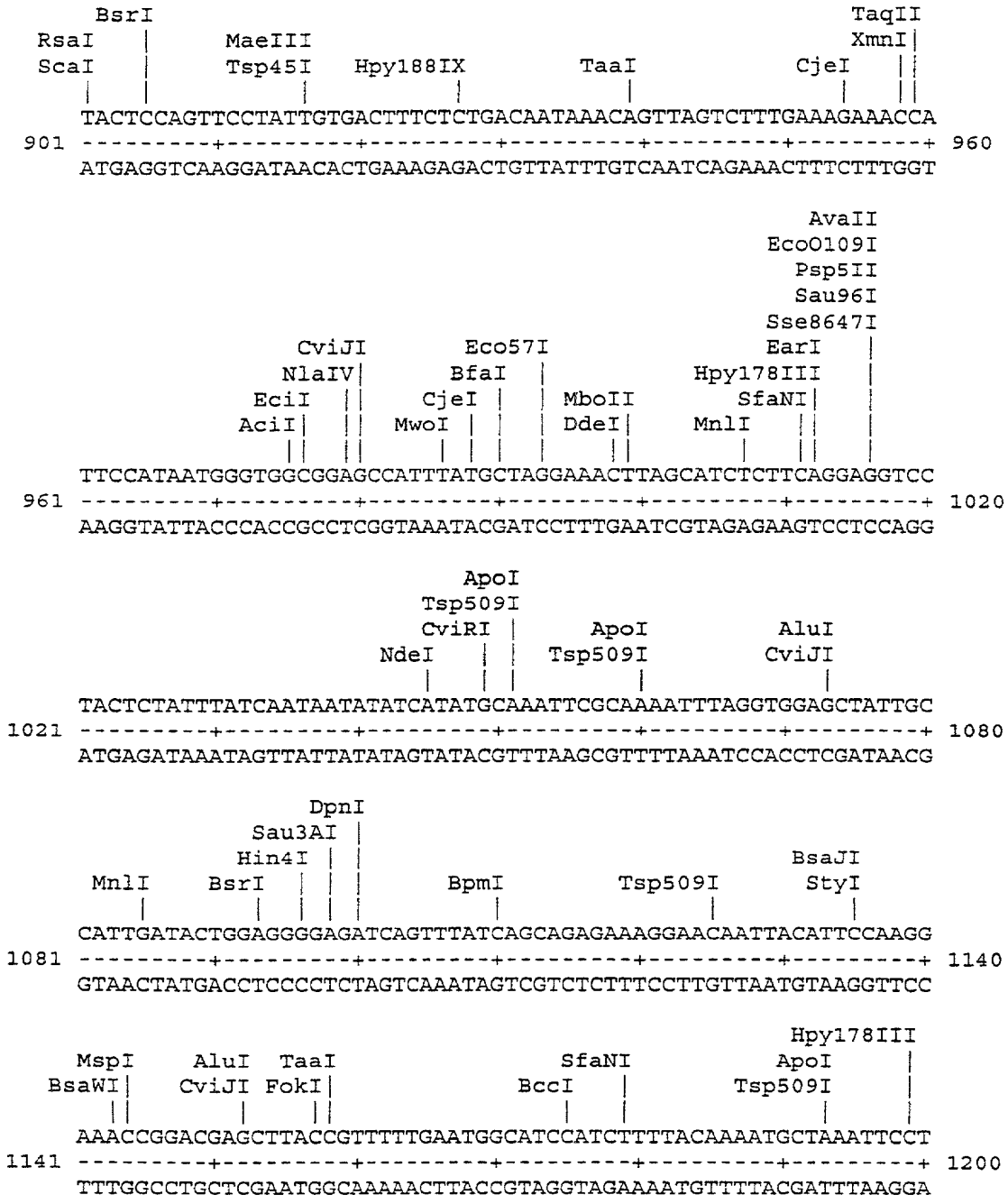

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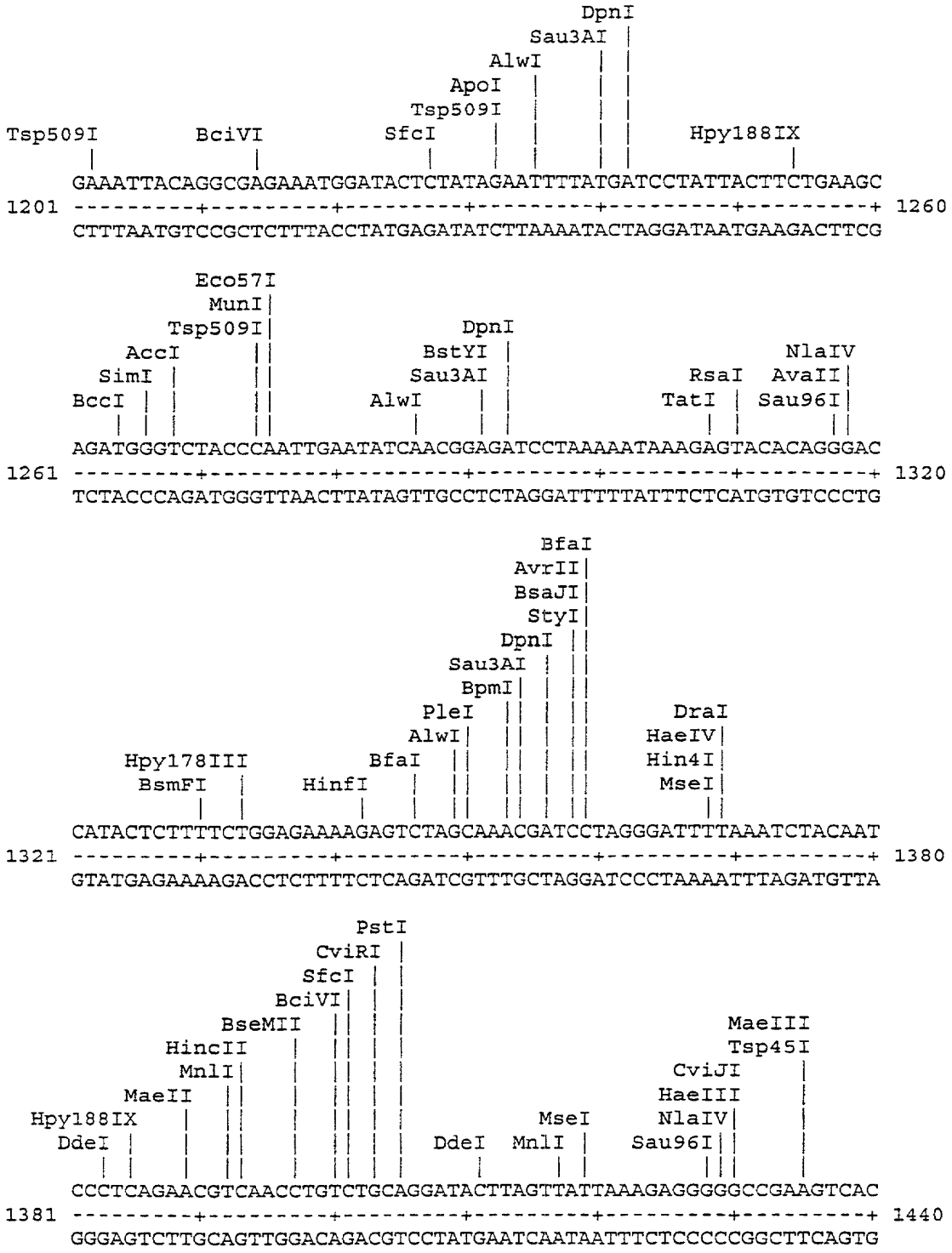

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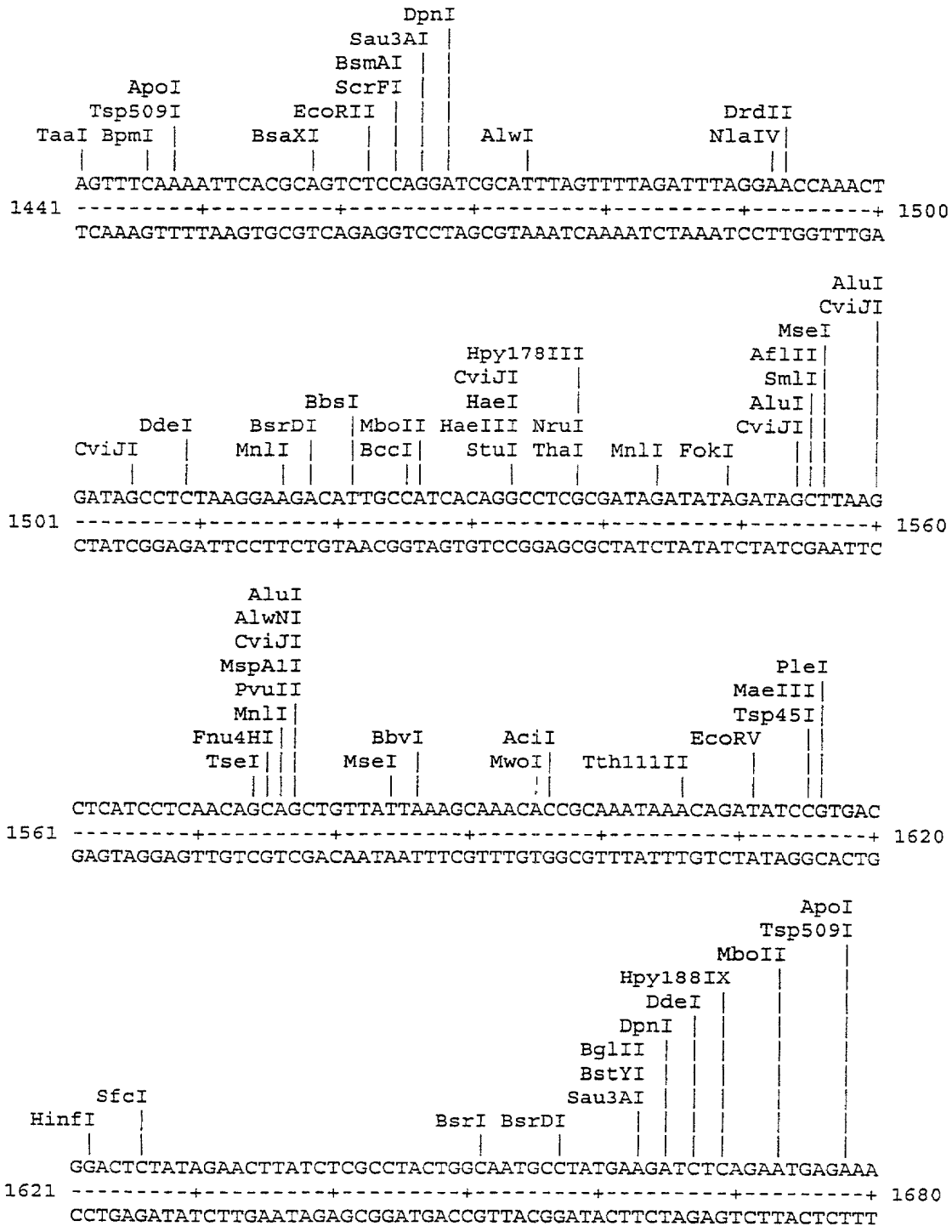

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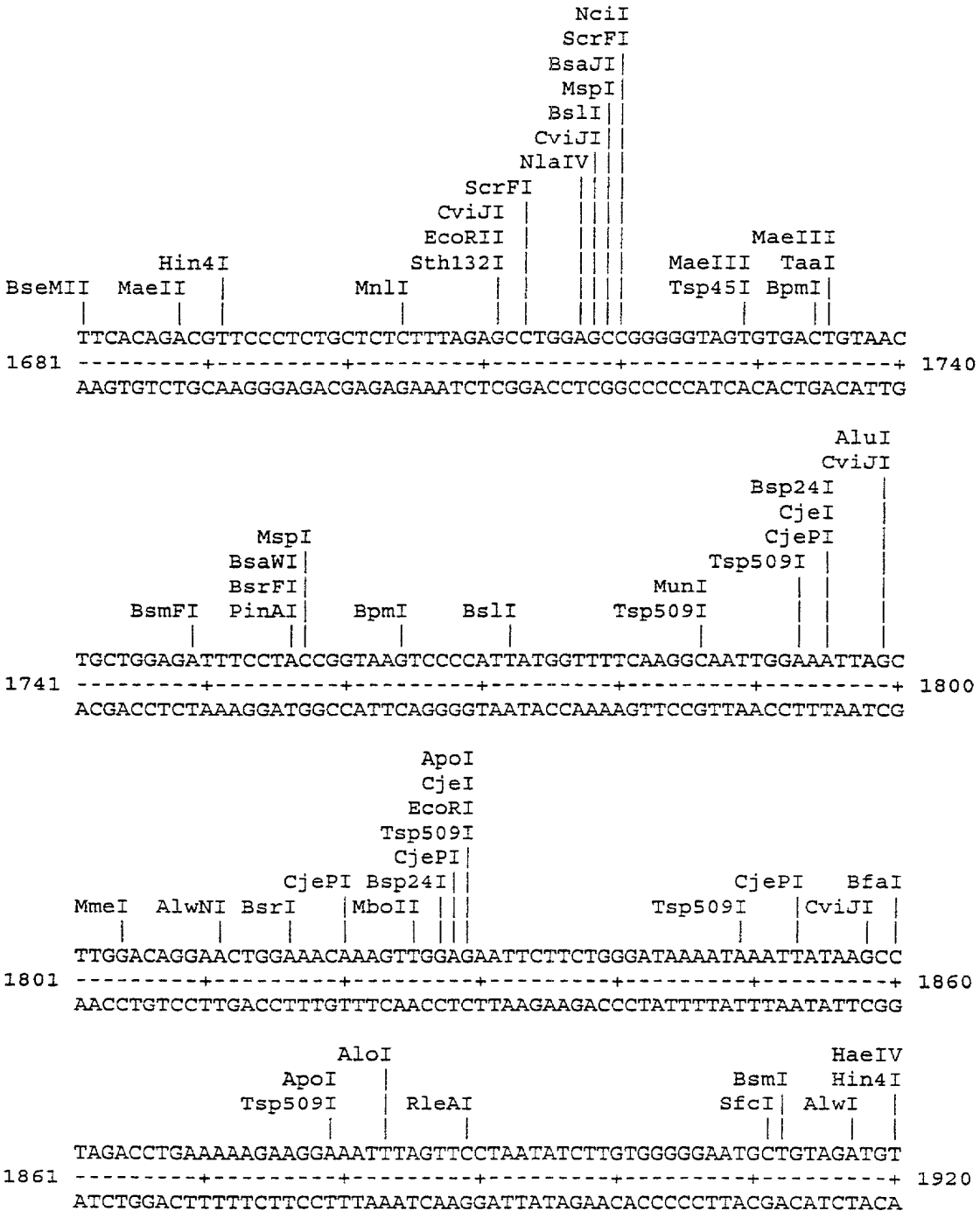

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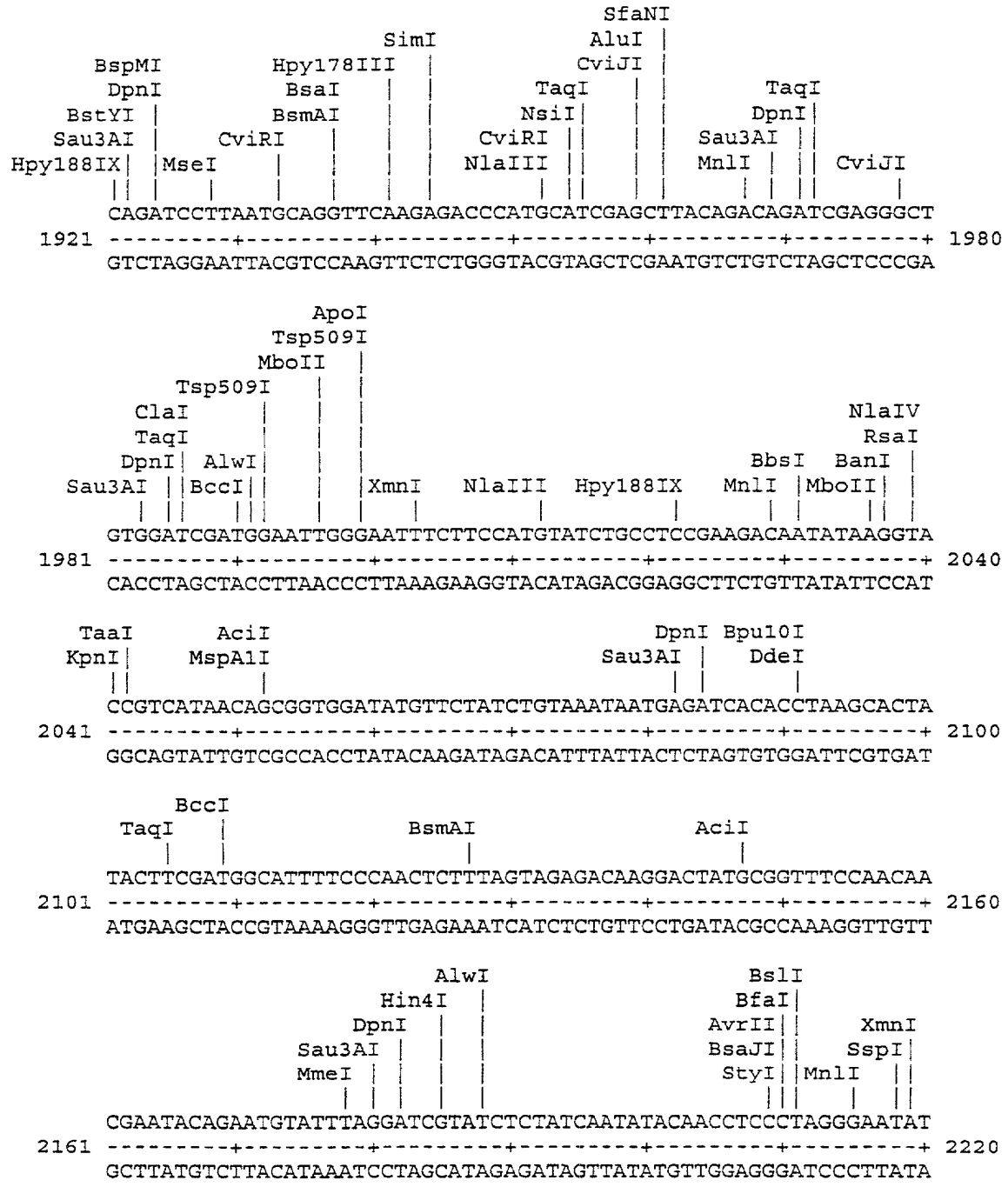
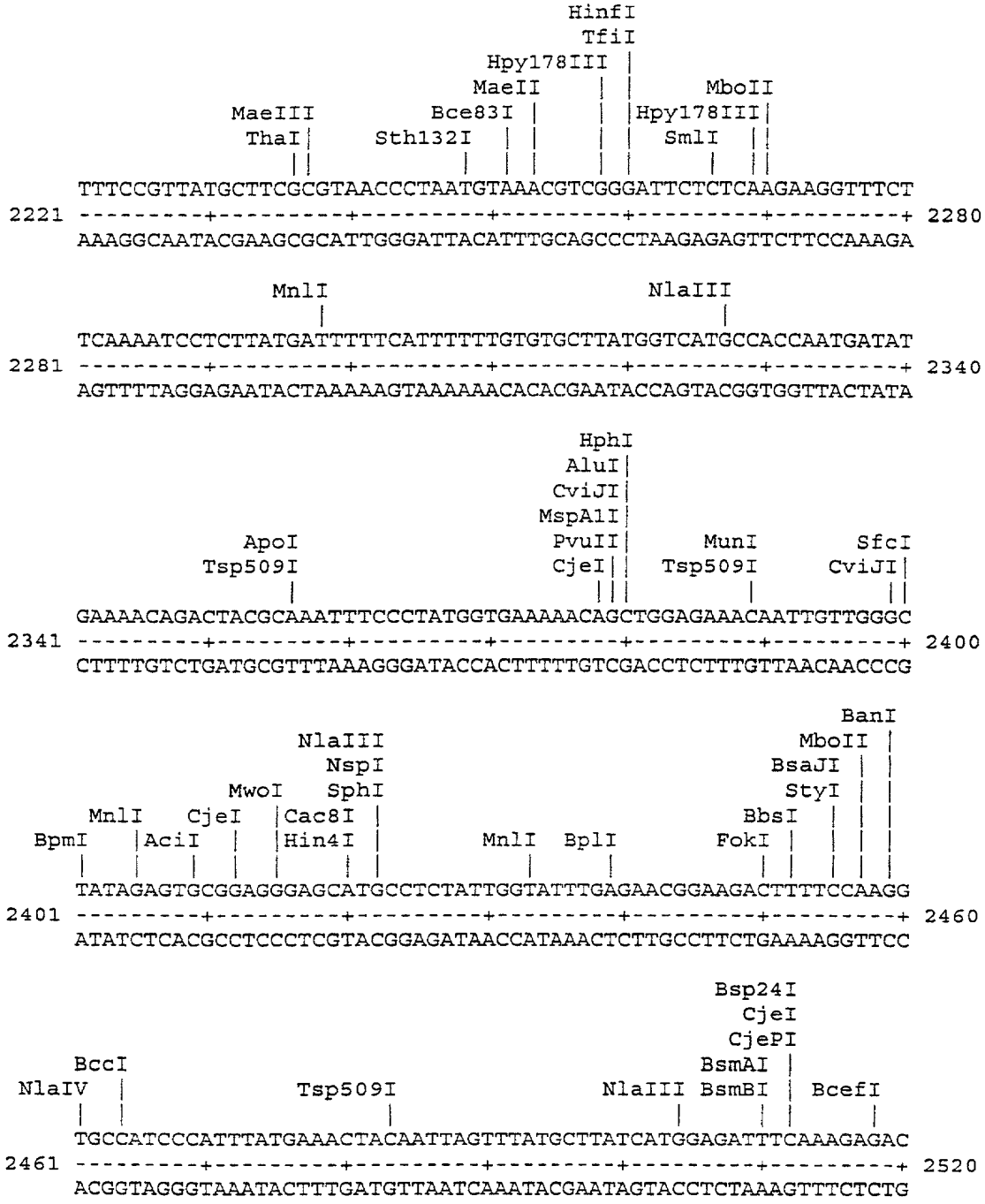


Figure 6 (continued)



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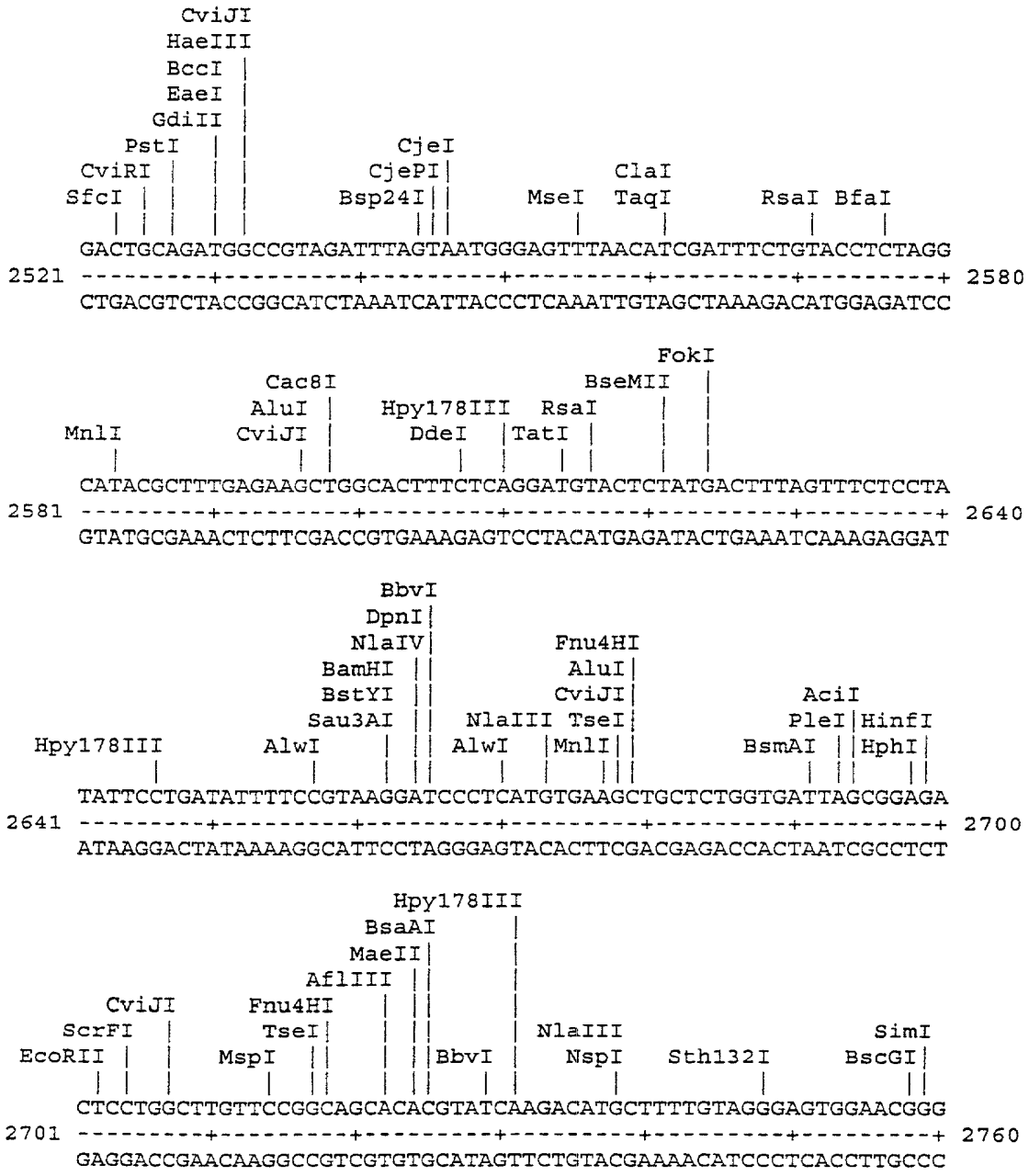

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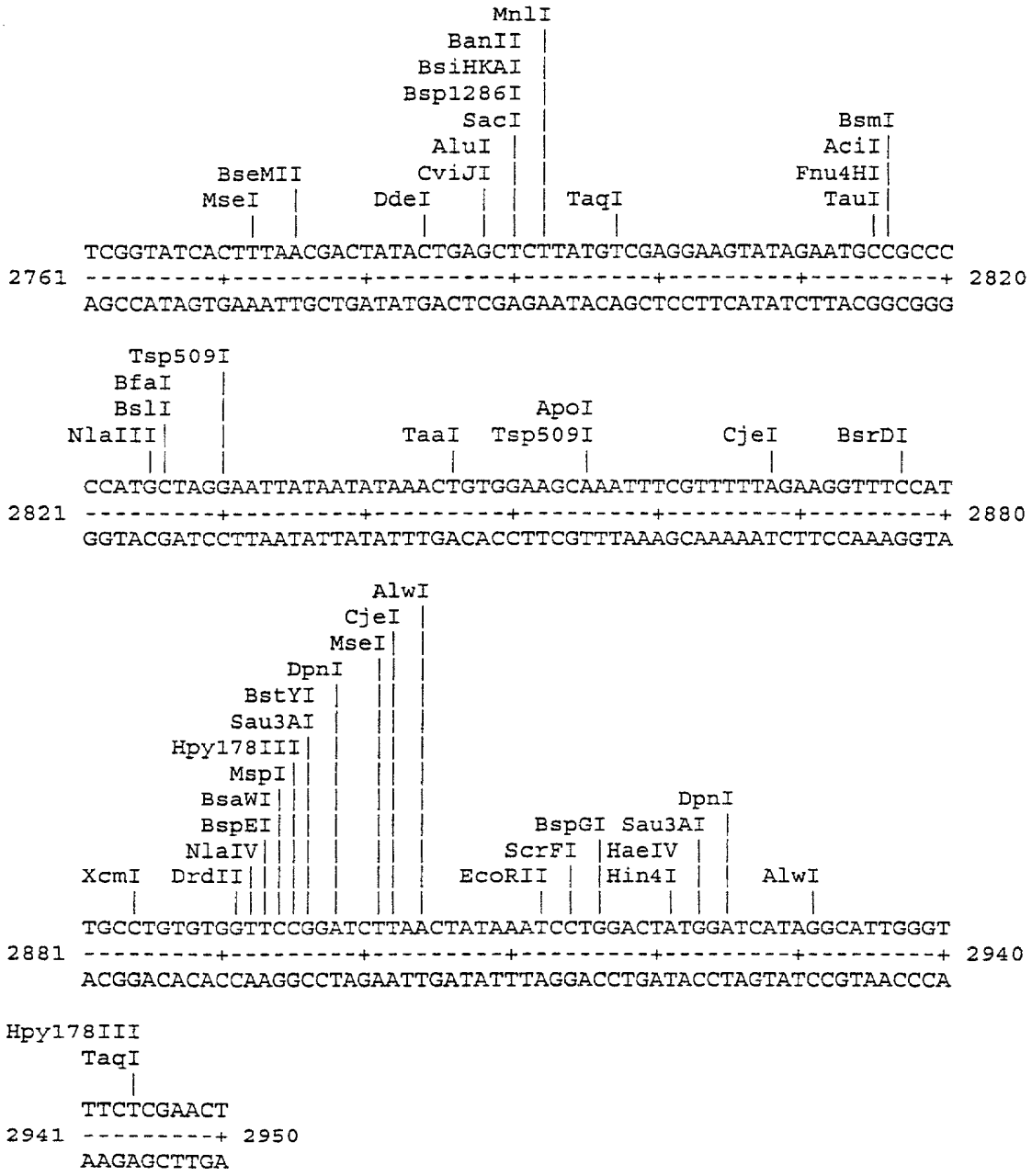


Figure 7

Restriction enzyme analysis of CPN100325 (RY 62 - SEQ ID NO. 7)

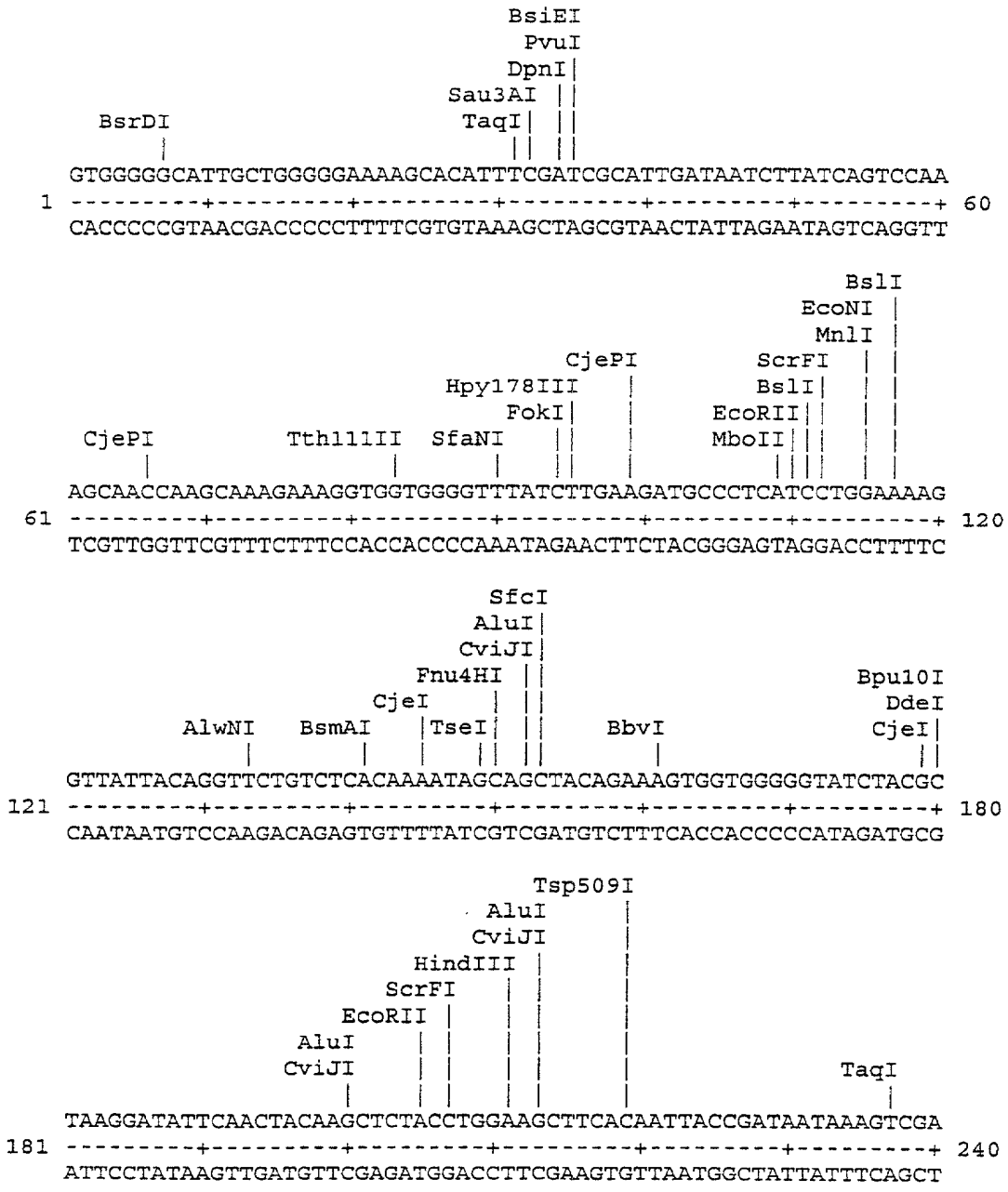


Figure 7 (continued)

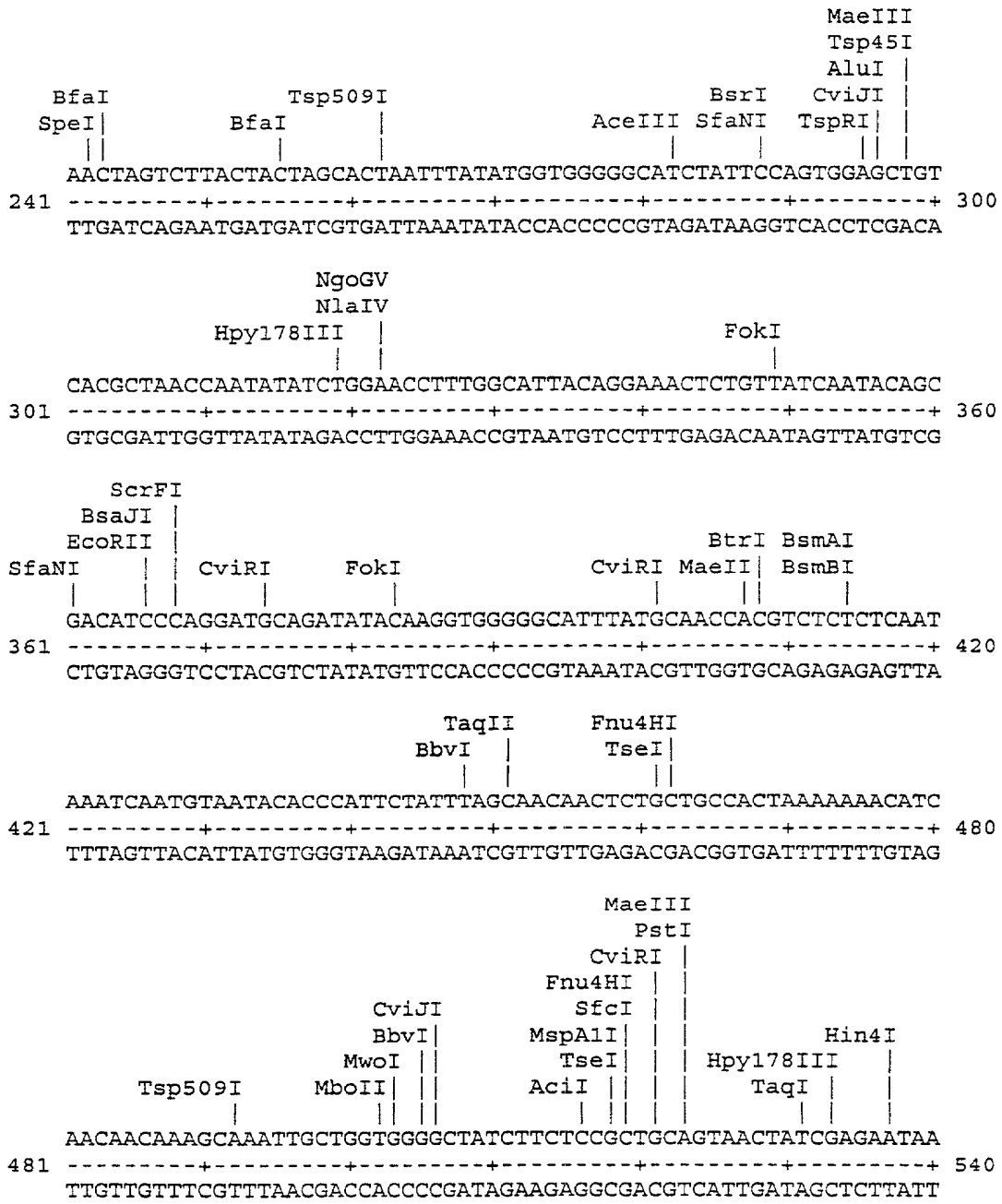
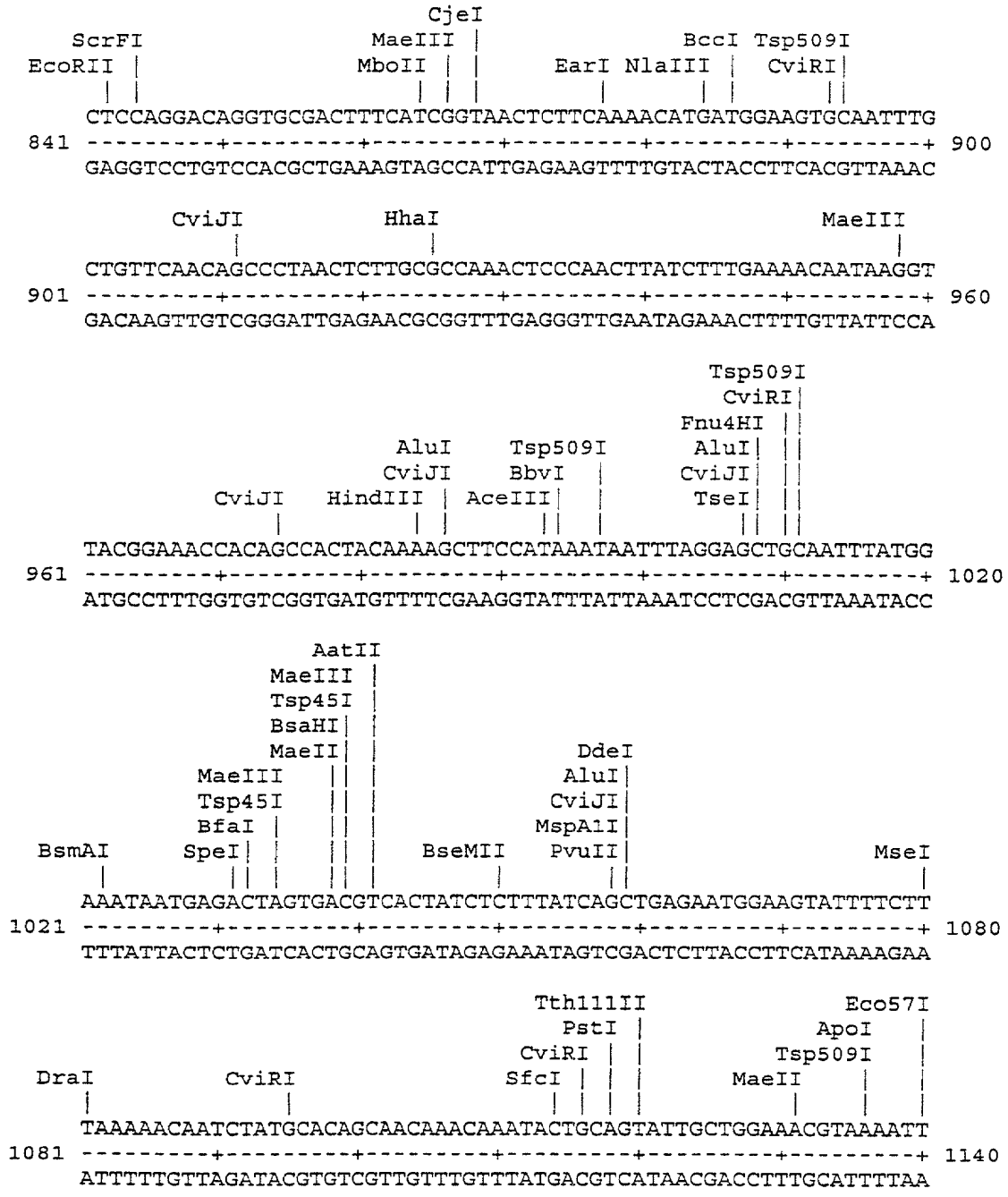


Figure 7 (continued)

Figure 7 (continued)



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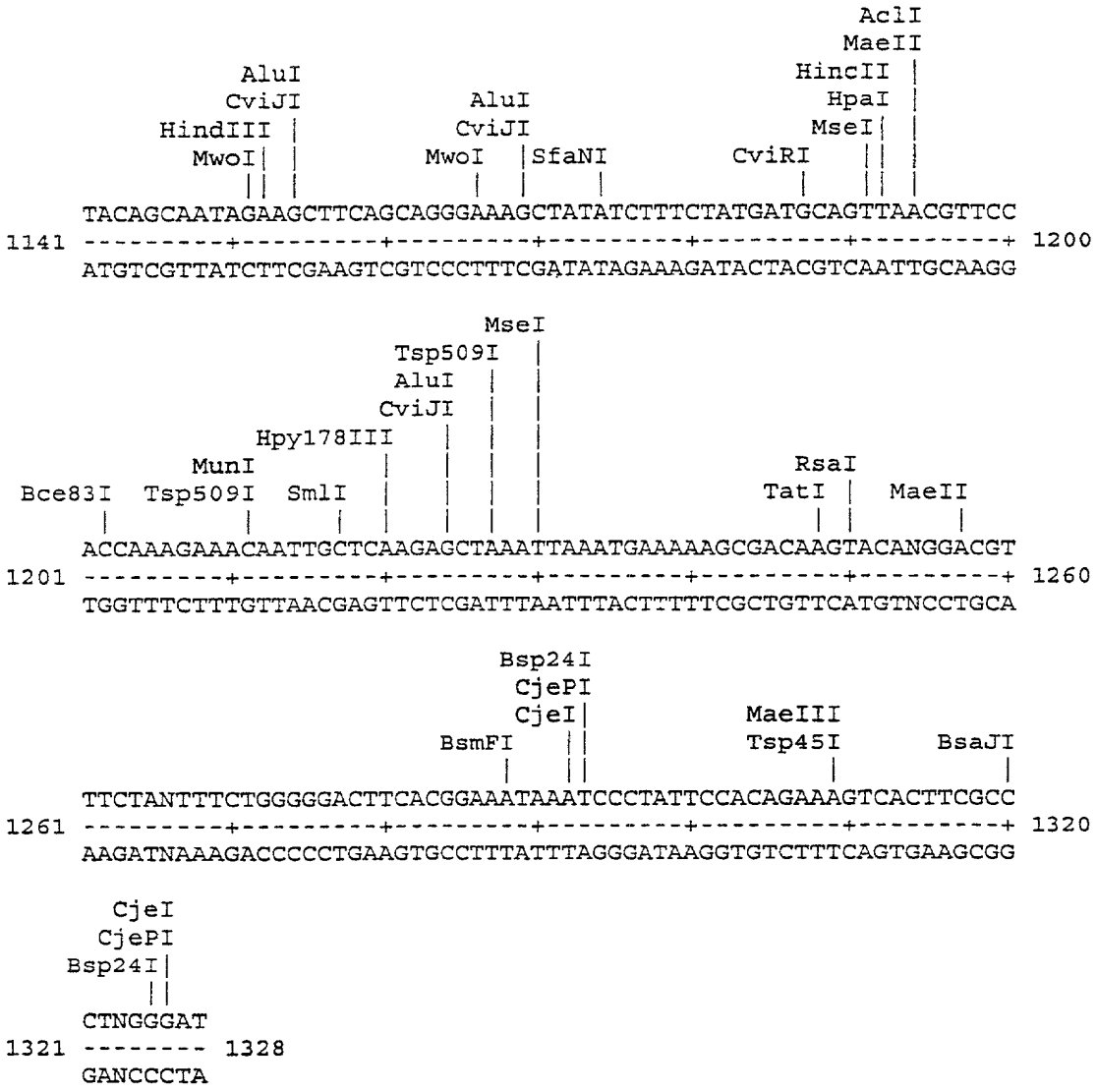
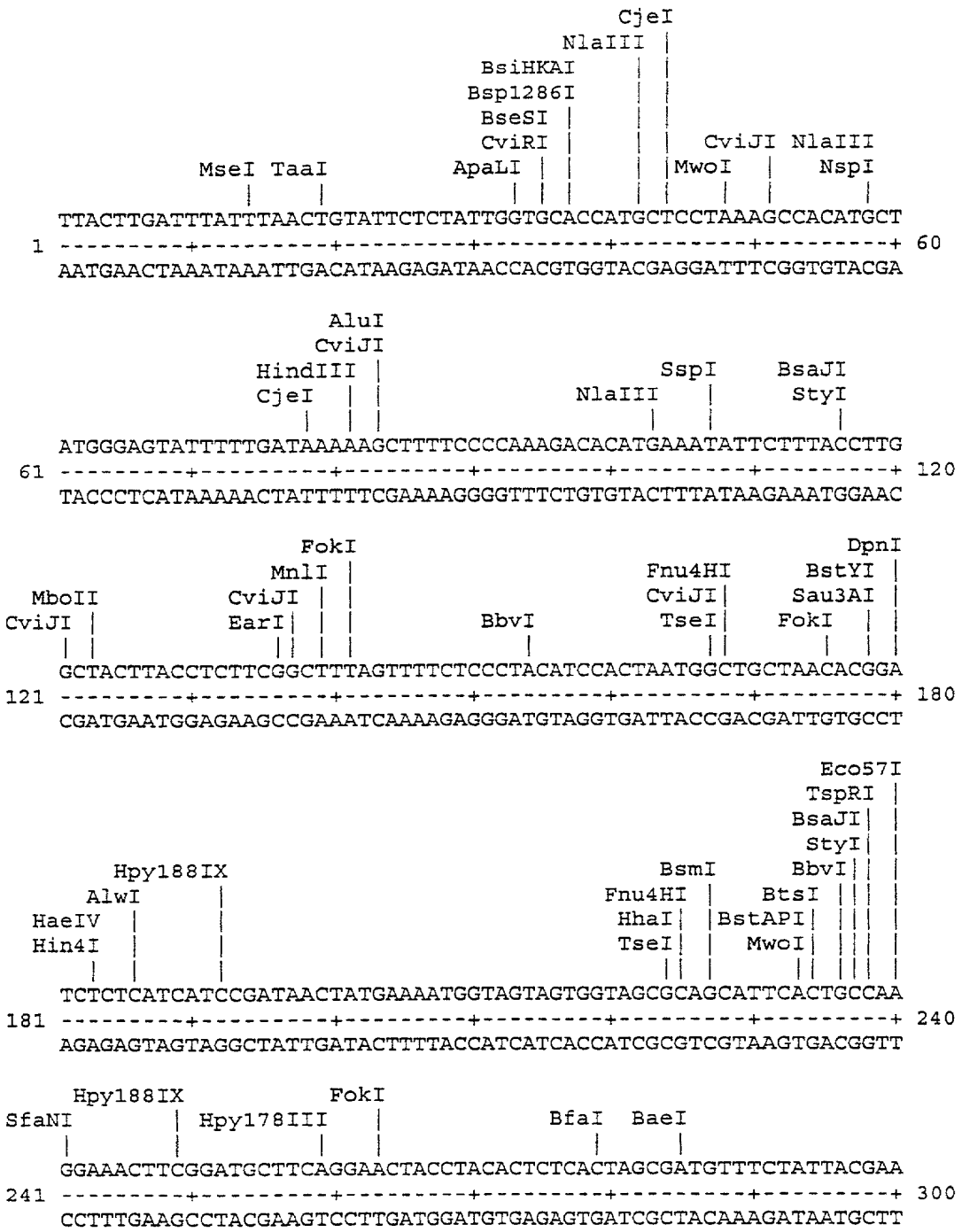


Figure 8

Restriction enzyme analysis of CPN100368 (RY 63 - SEQ ID NO. 8)



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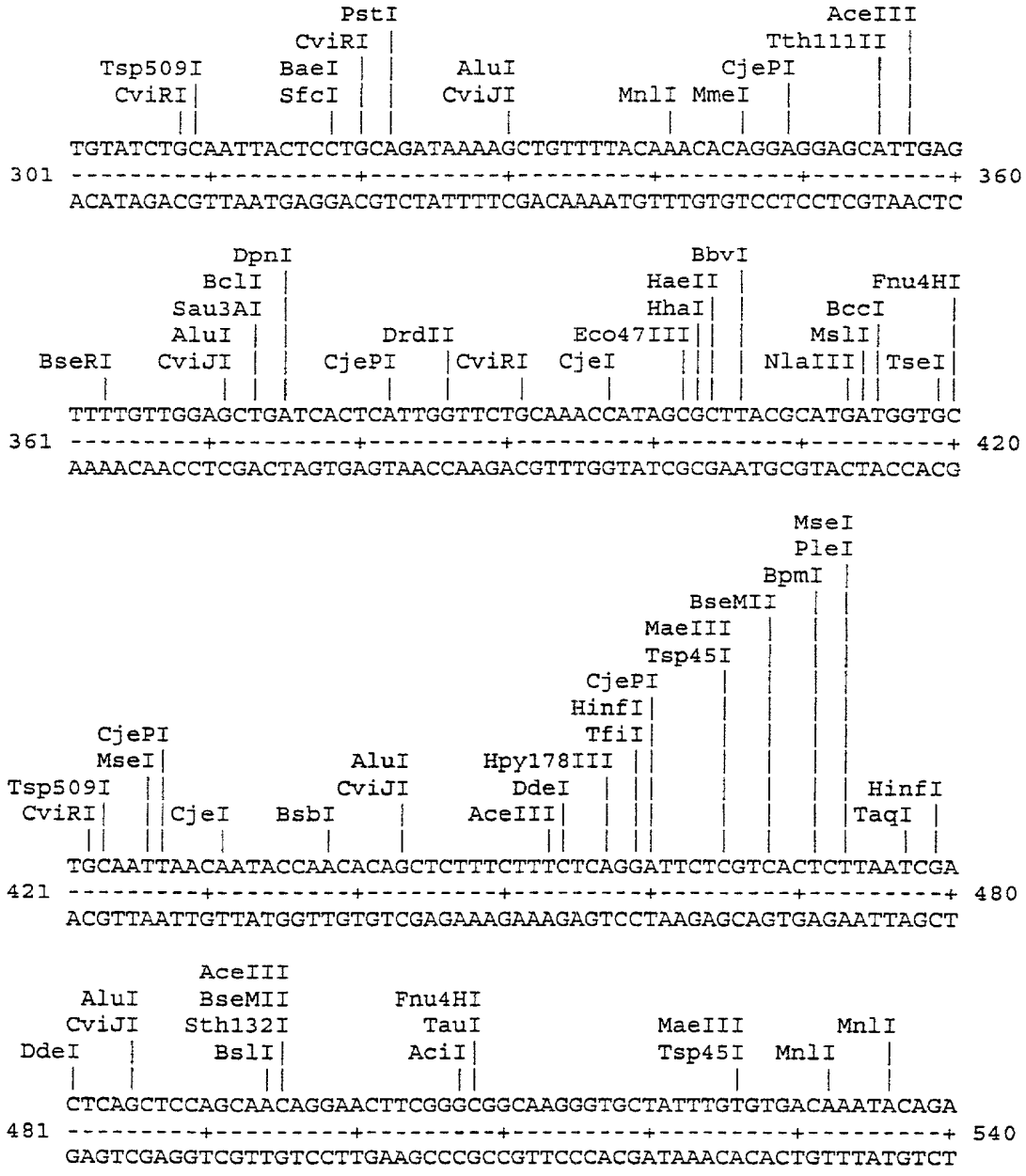

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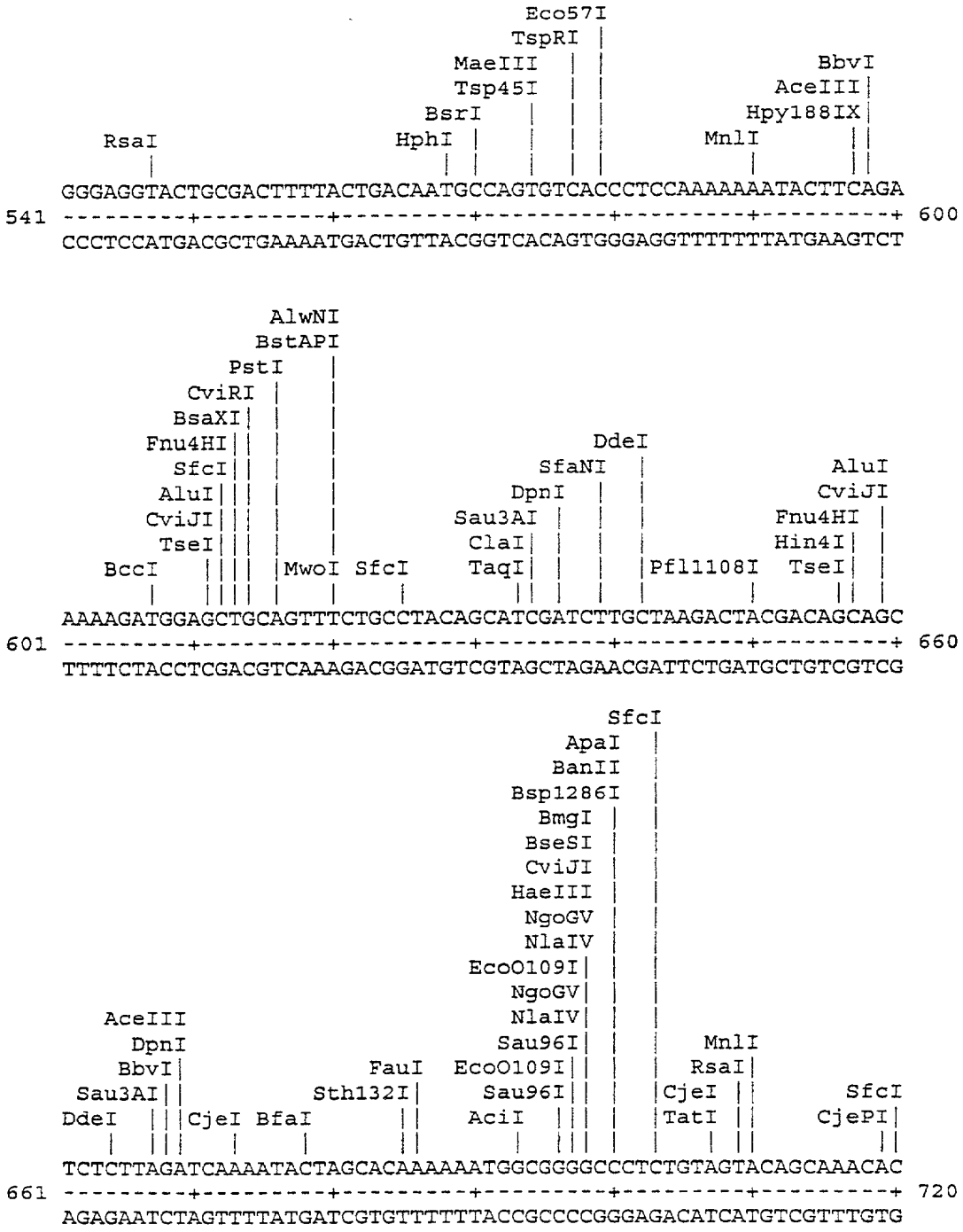

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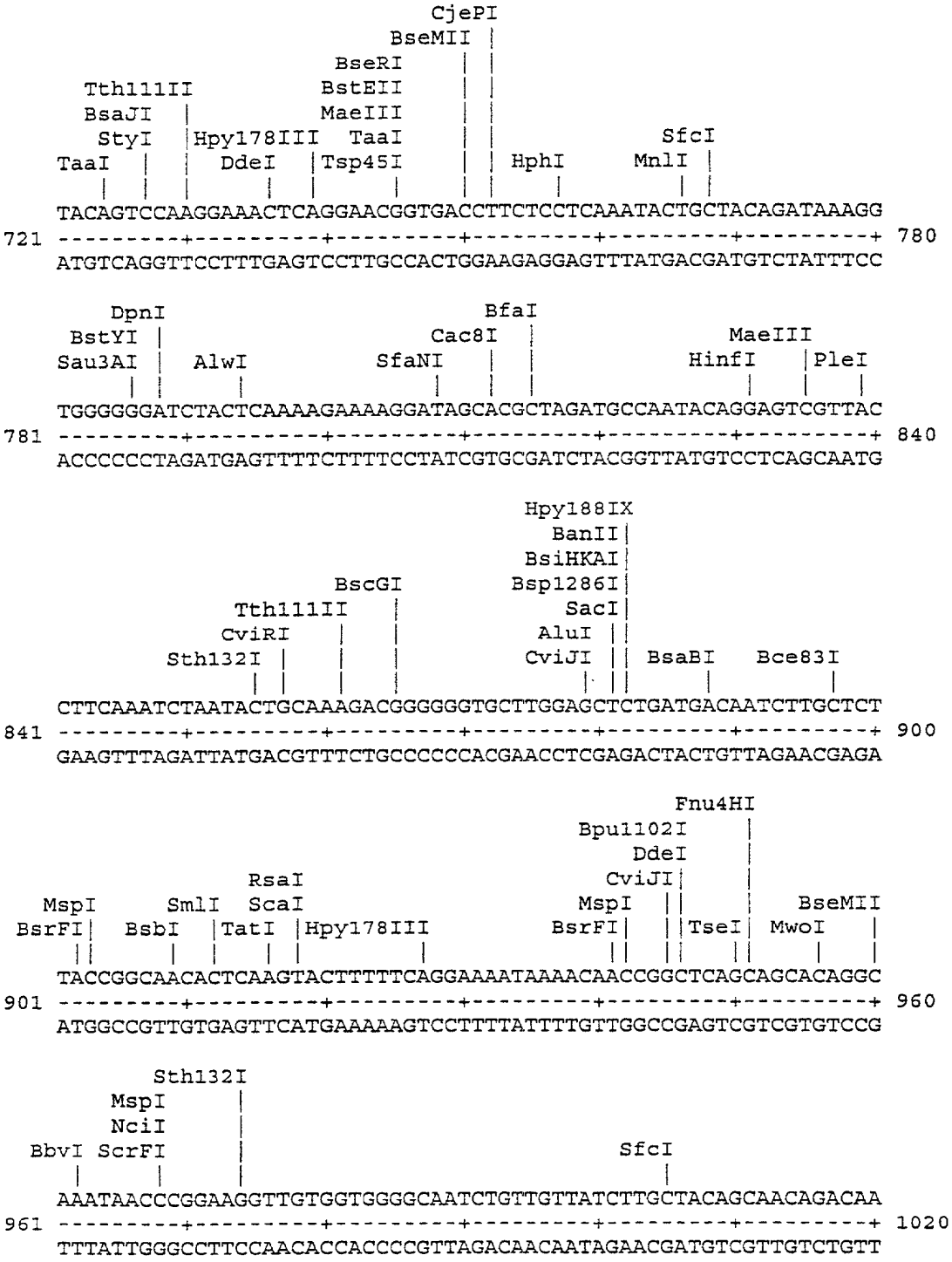

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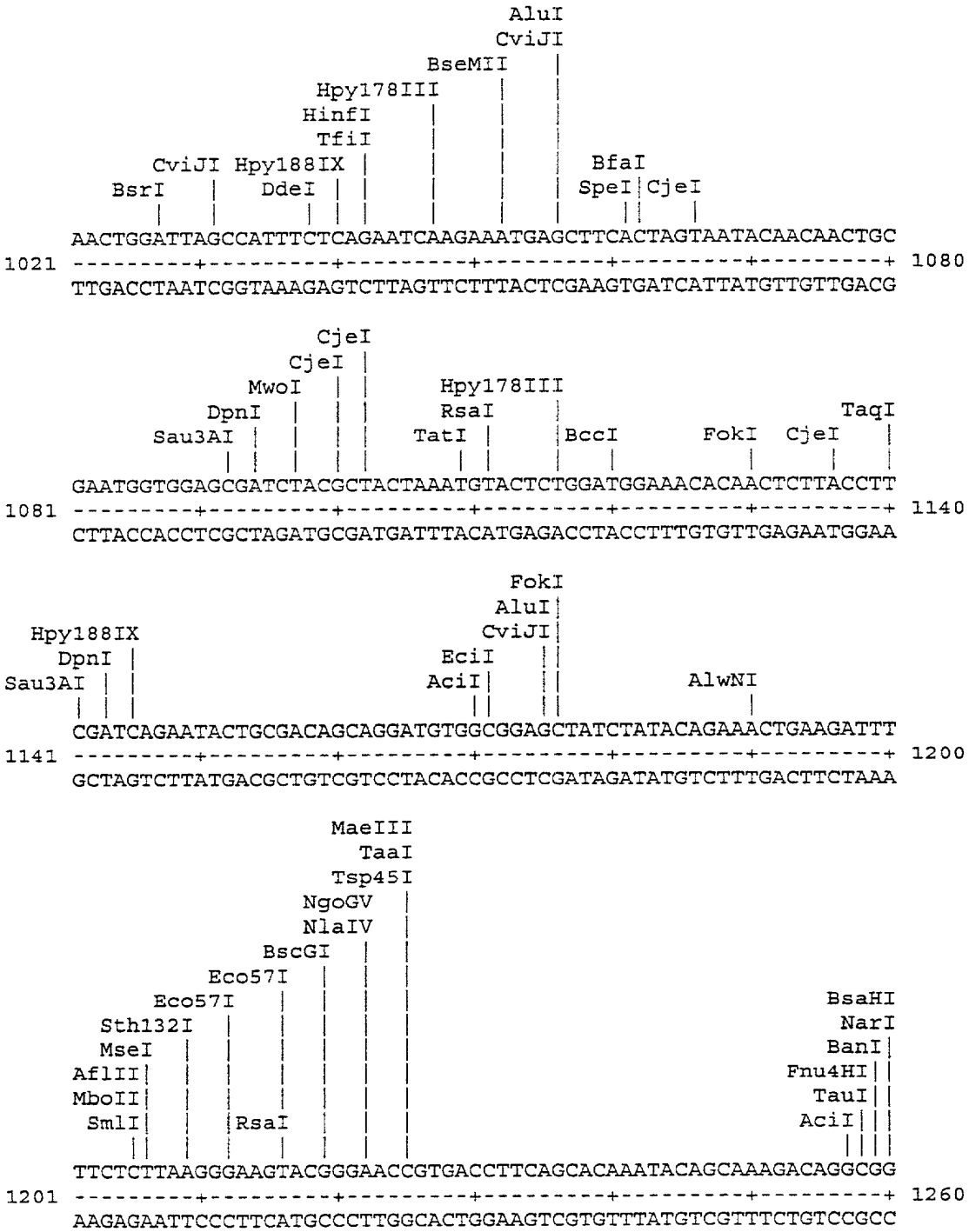

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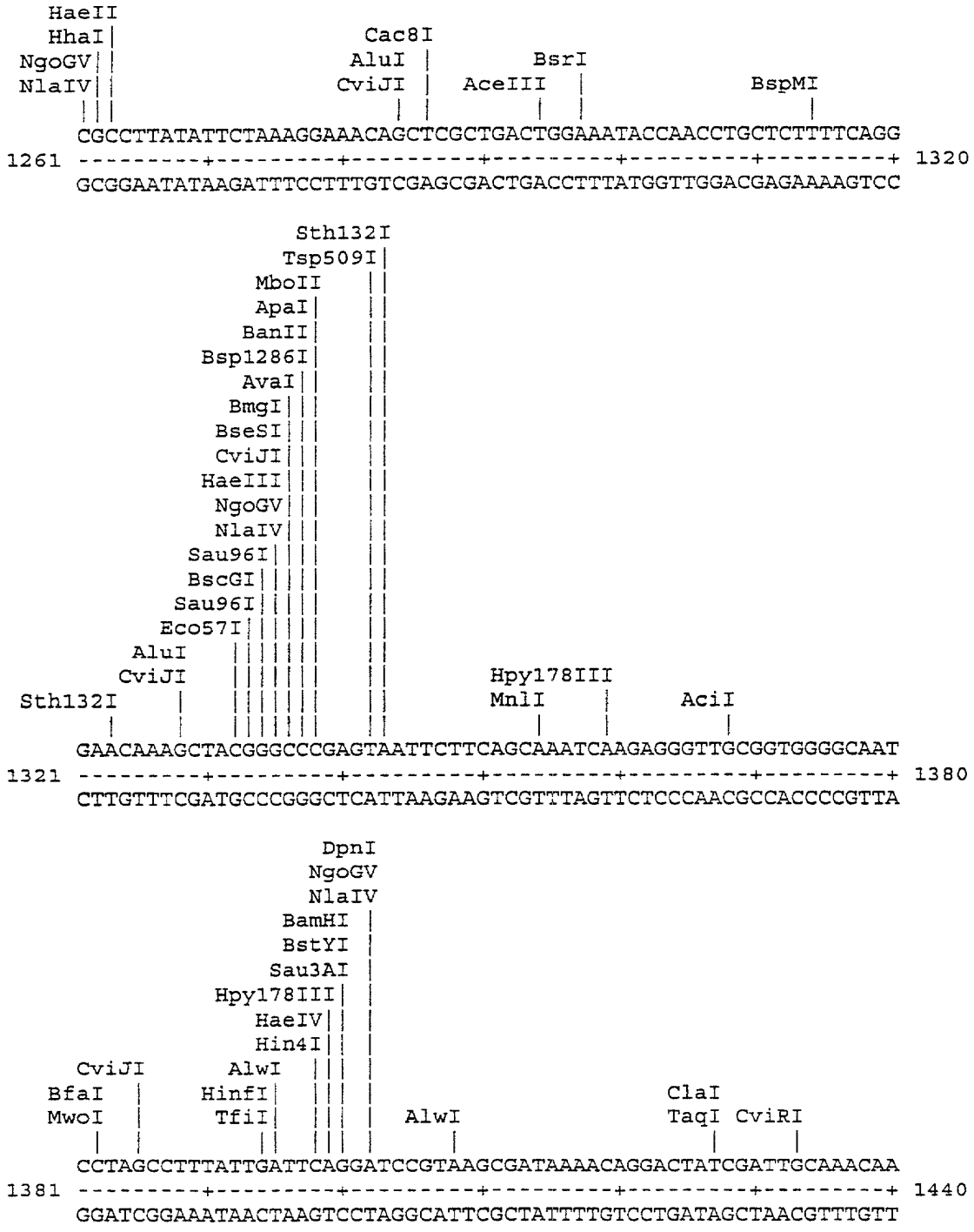

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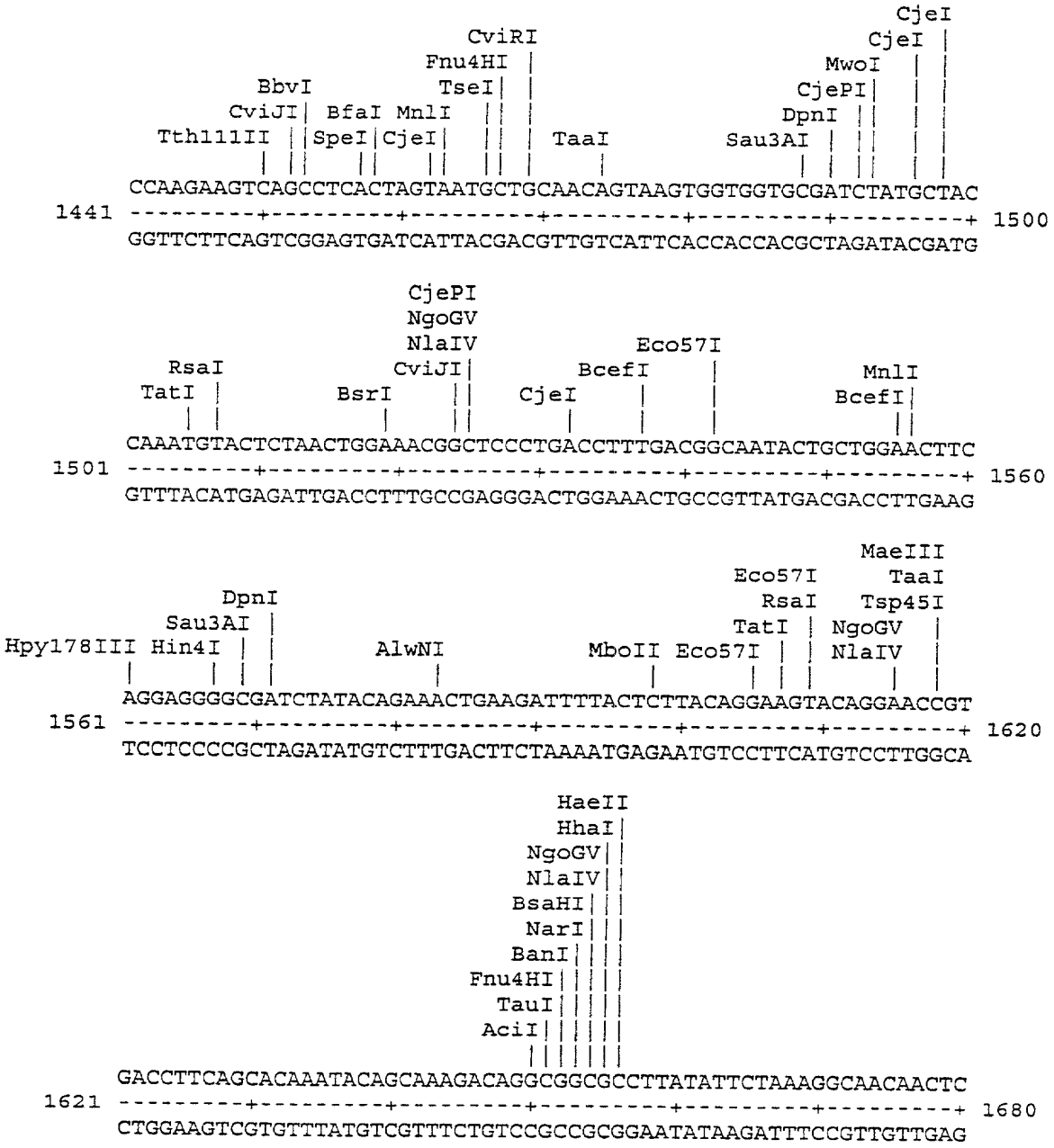

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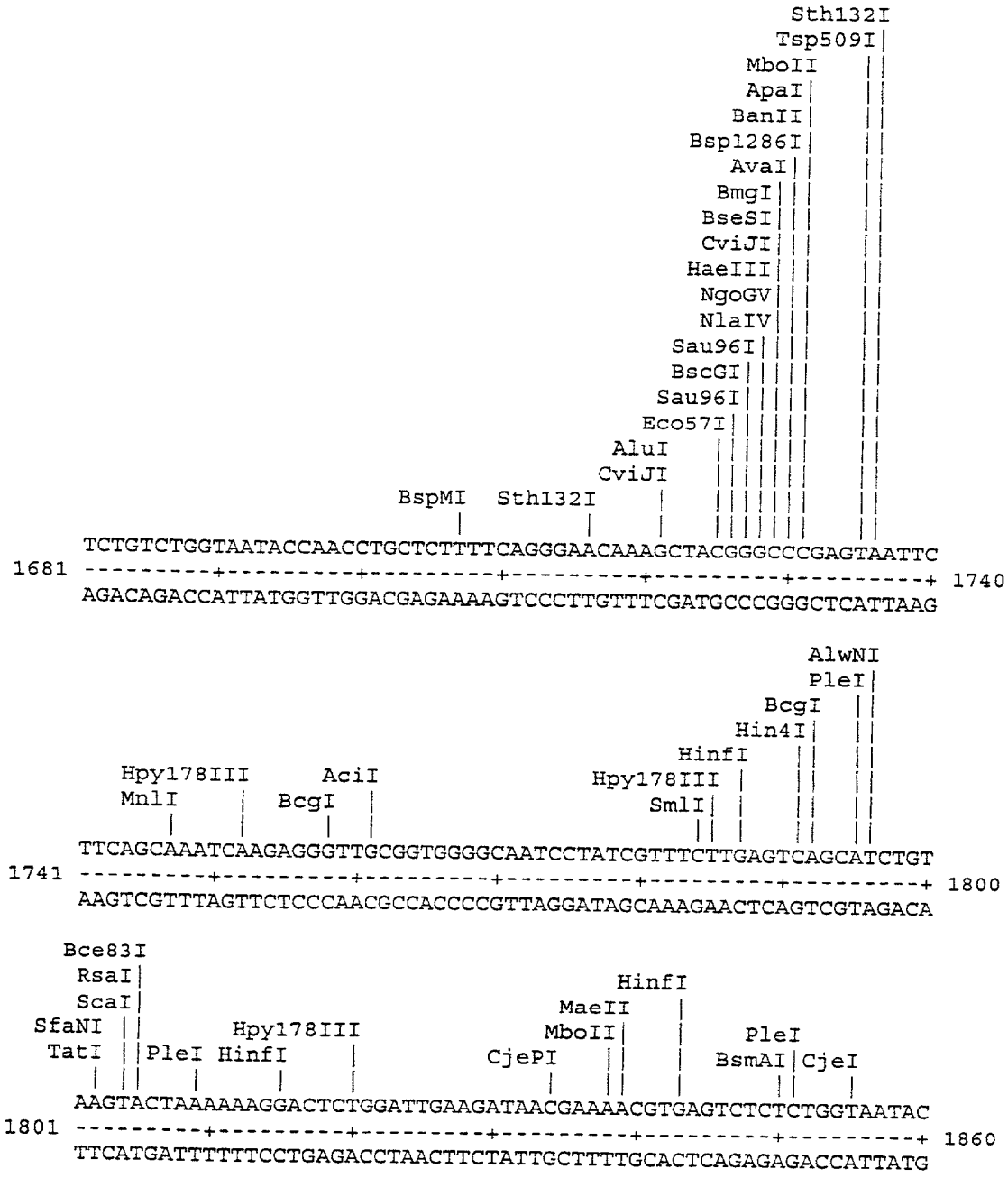

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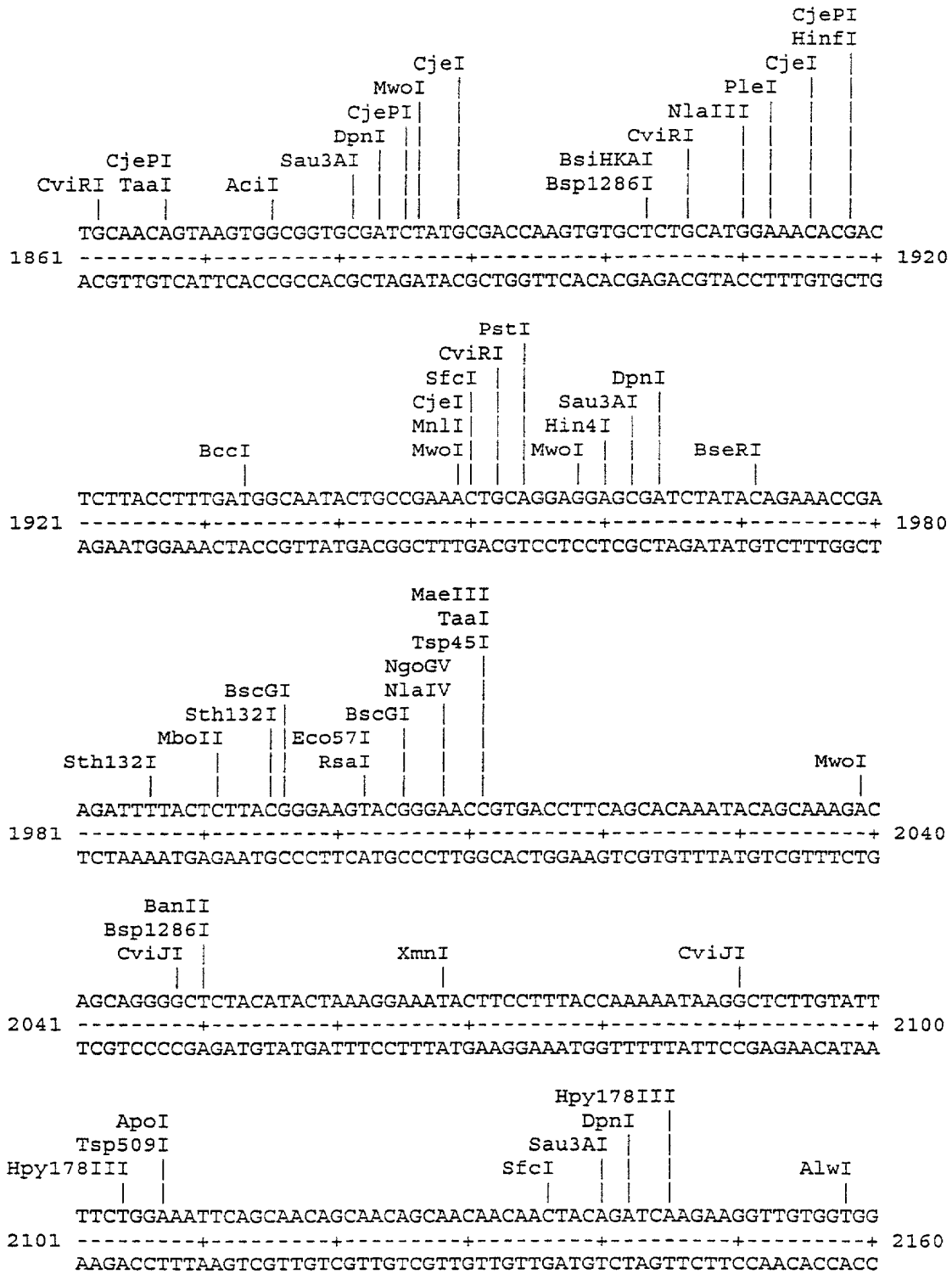

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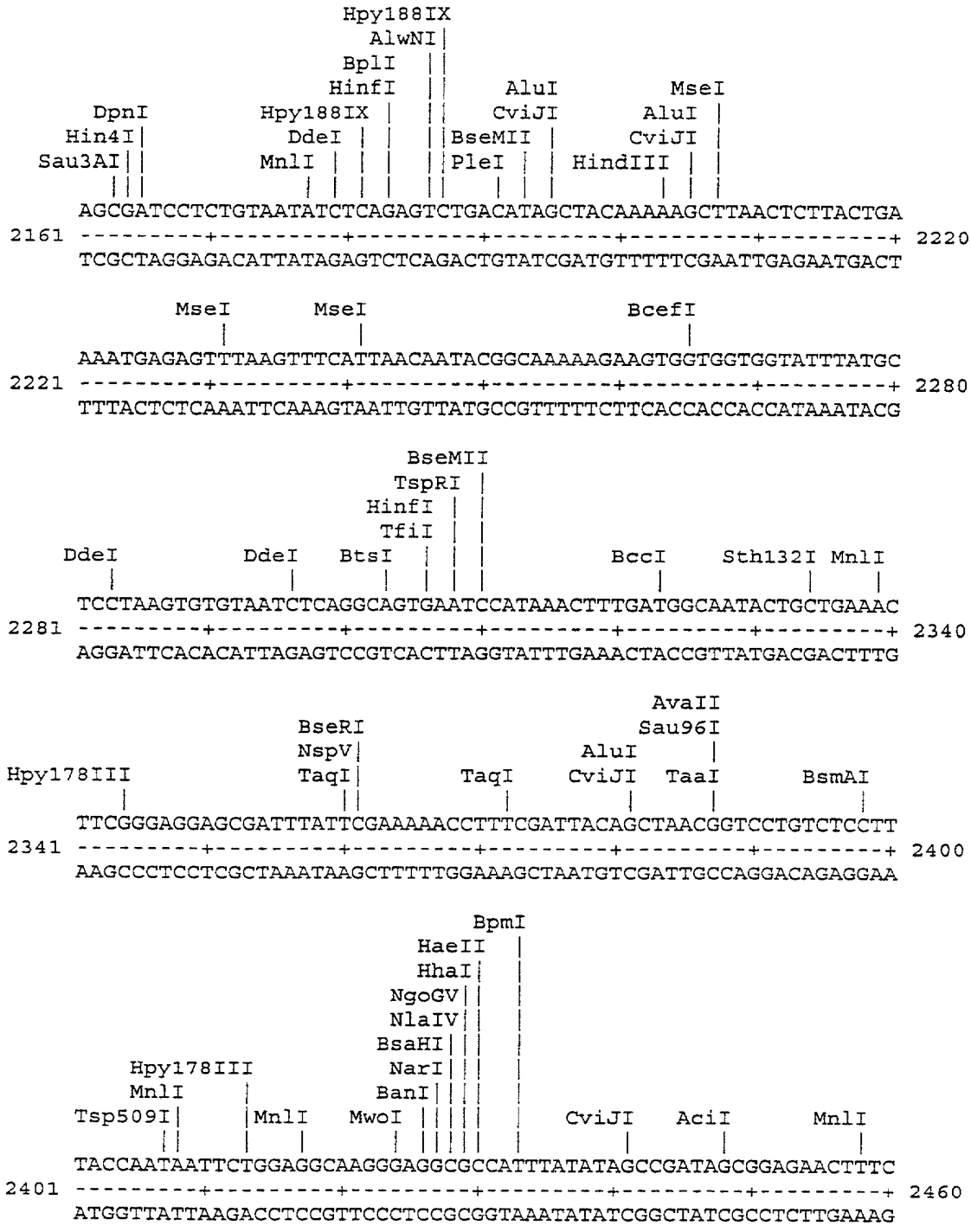

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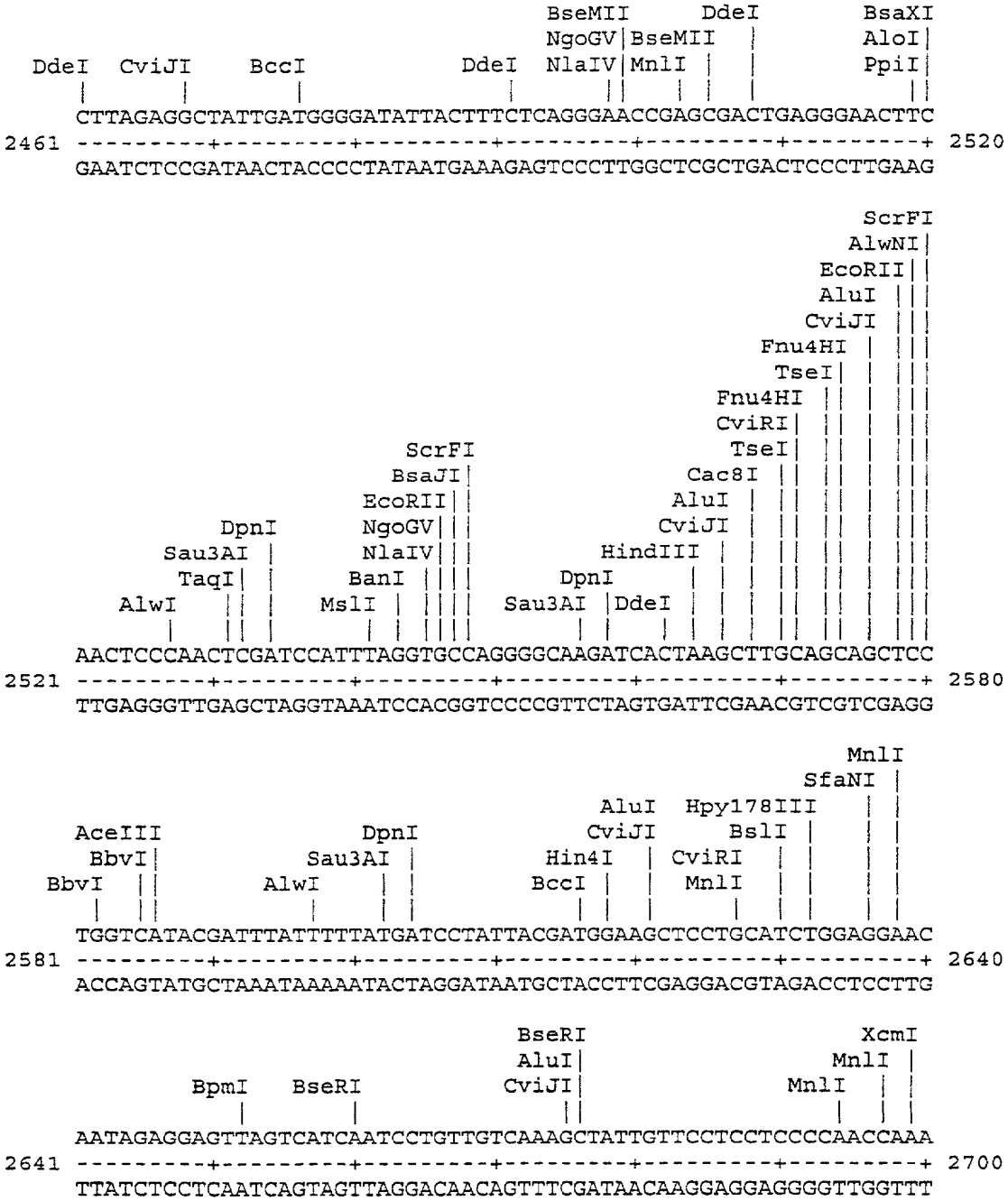

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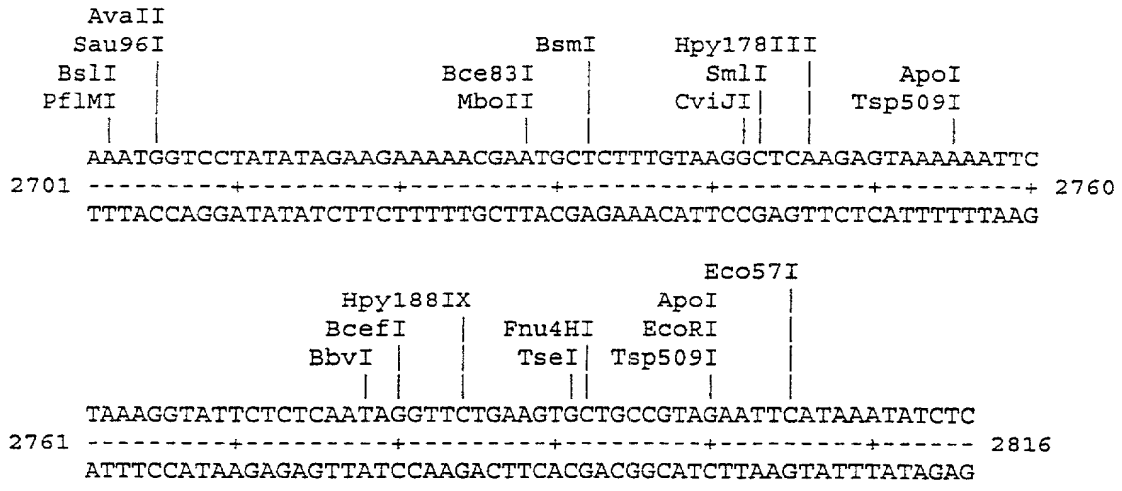
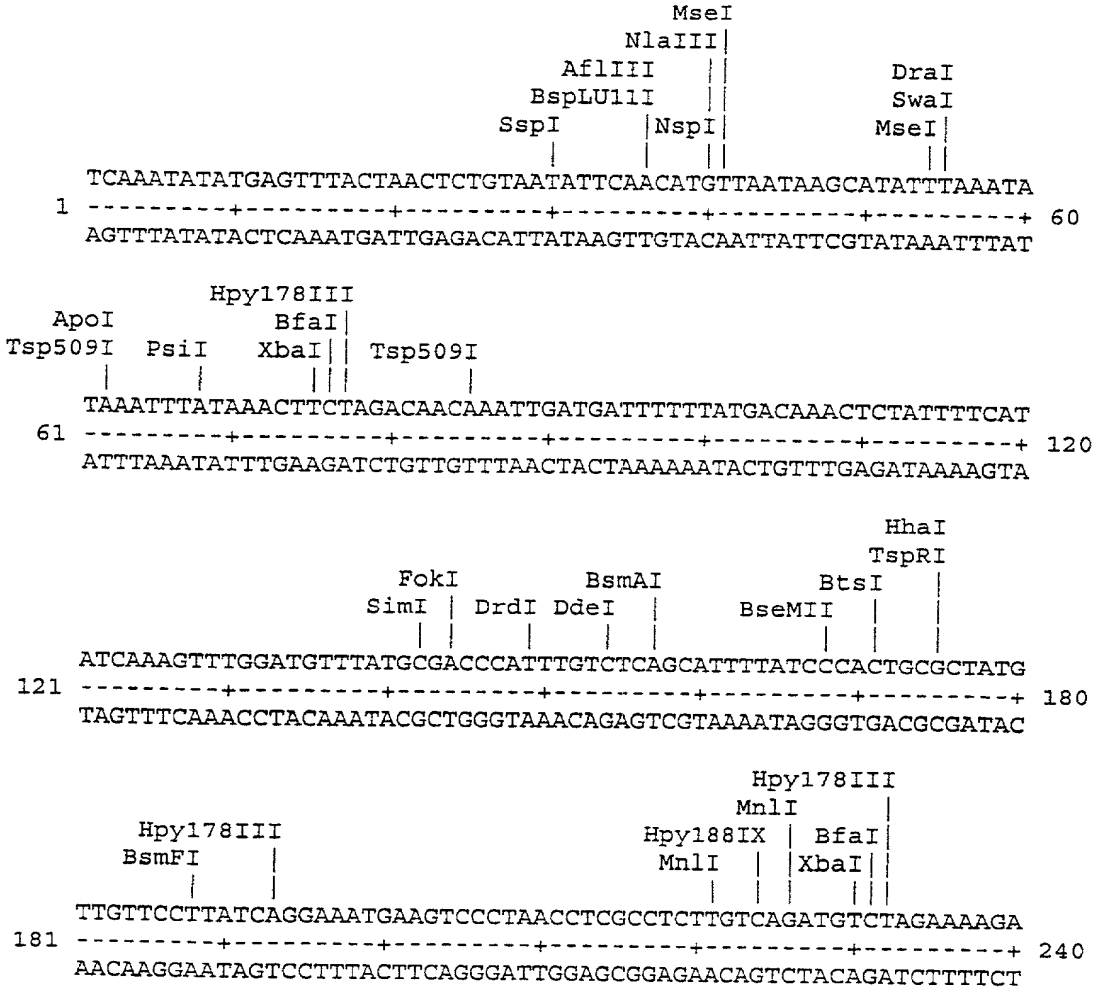


Figure 9
Restriction enzyme analysis of CPN100624 (RY 64 - SEQ ID NO. 9)



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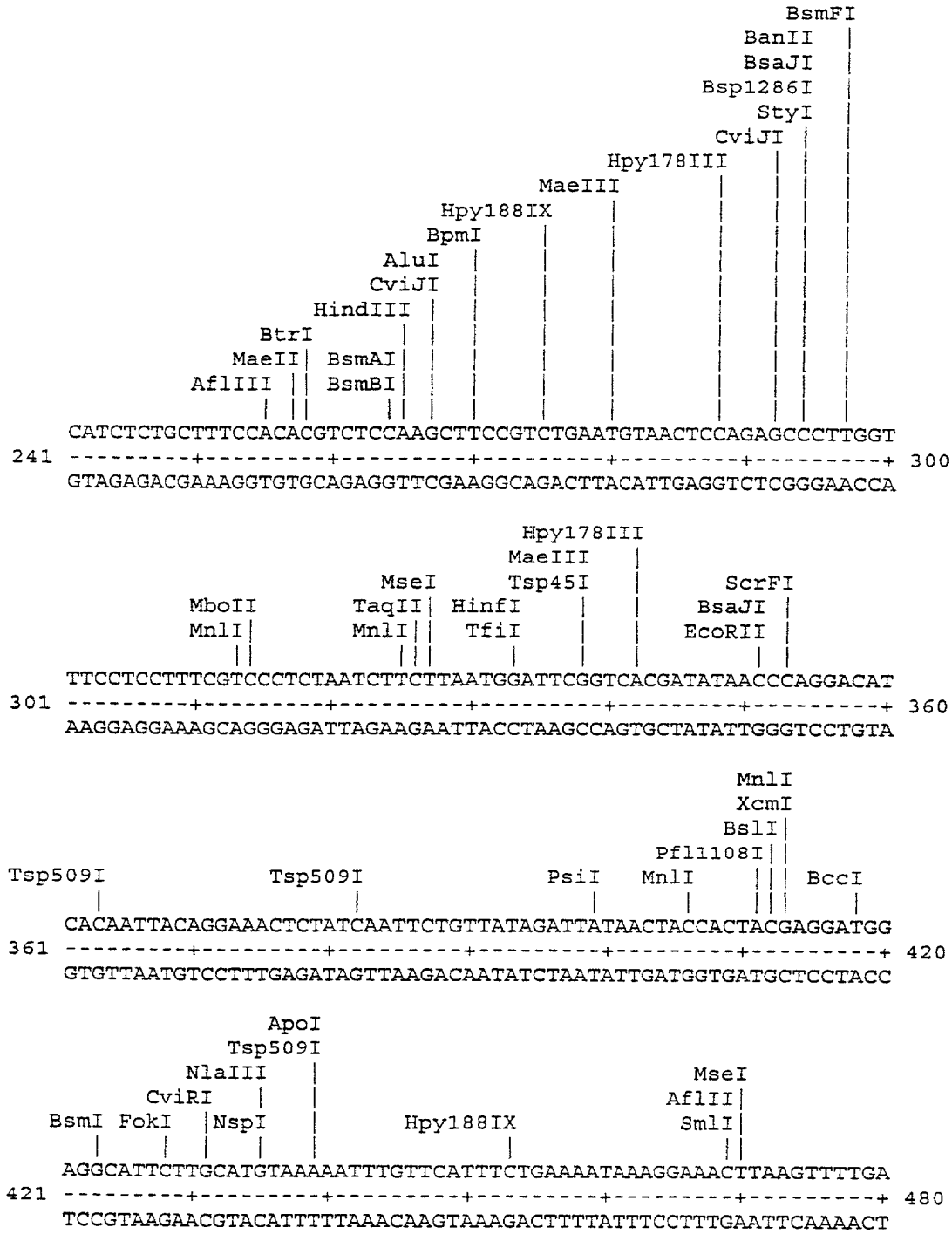

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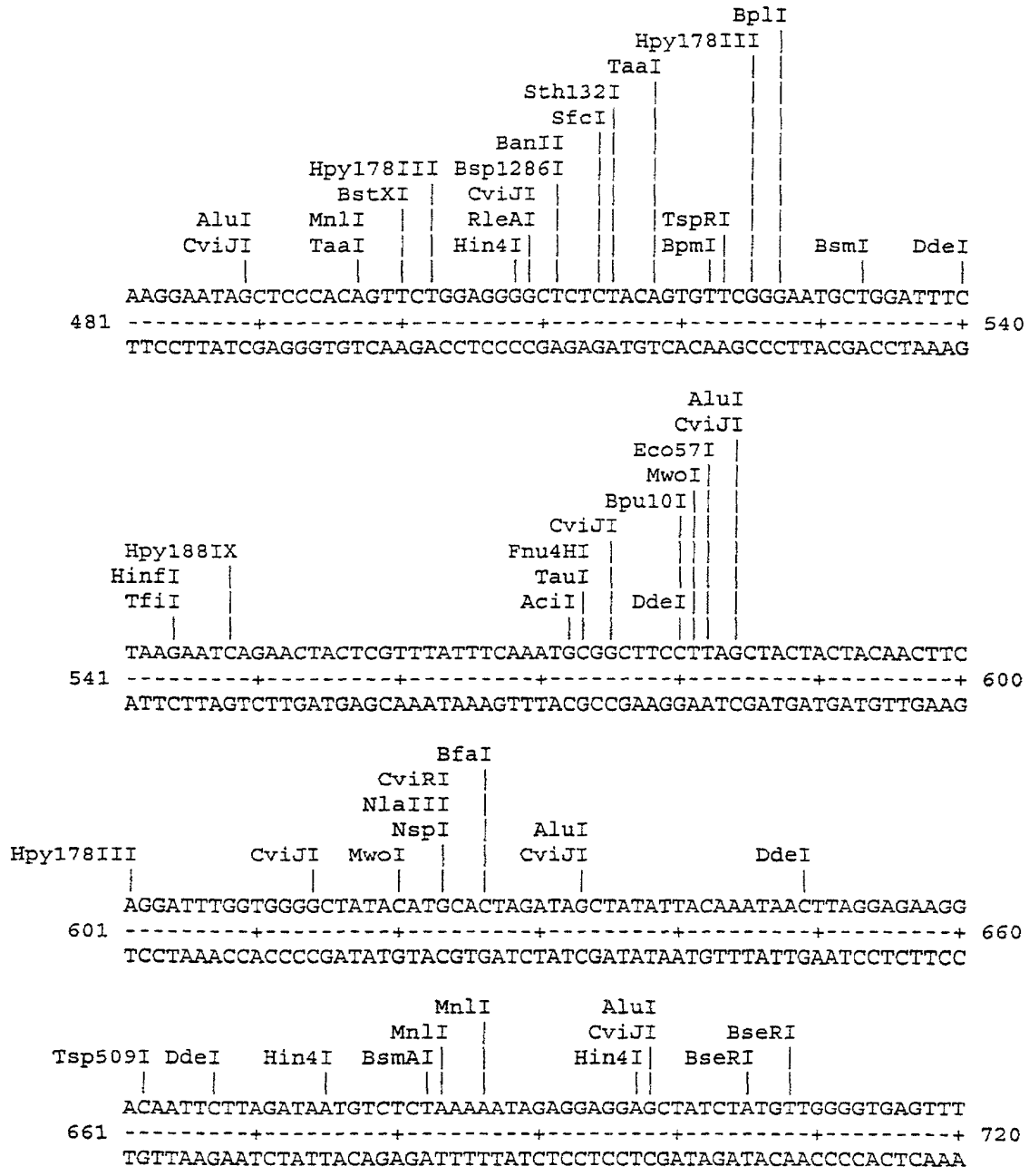

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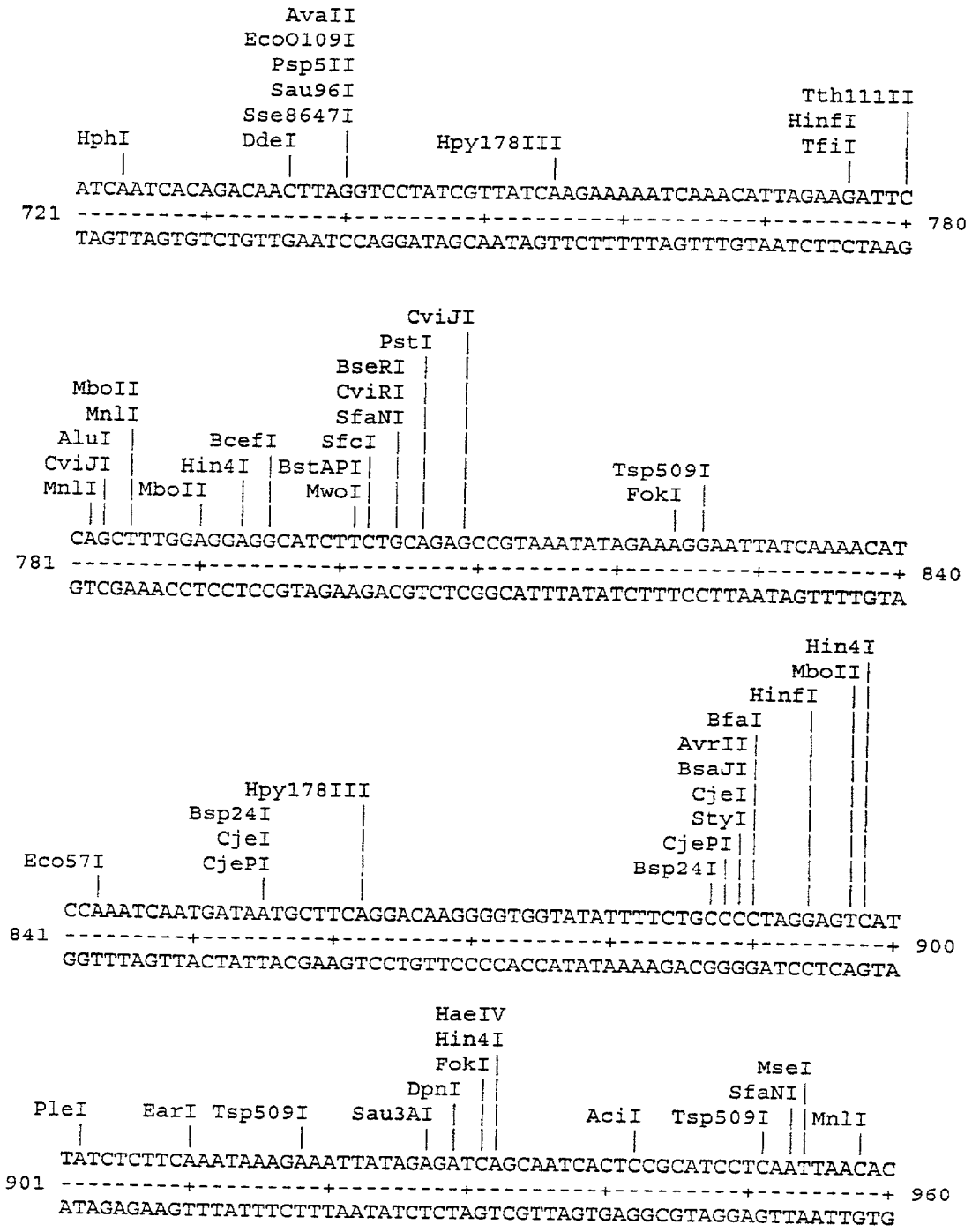

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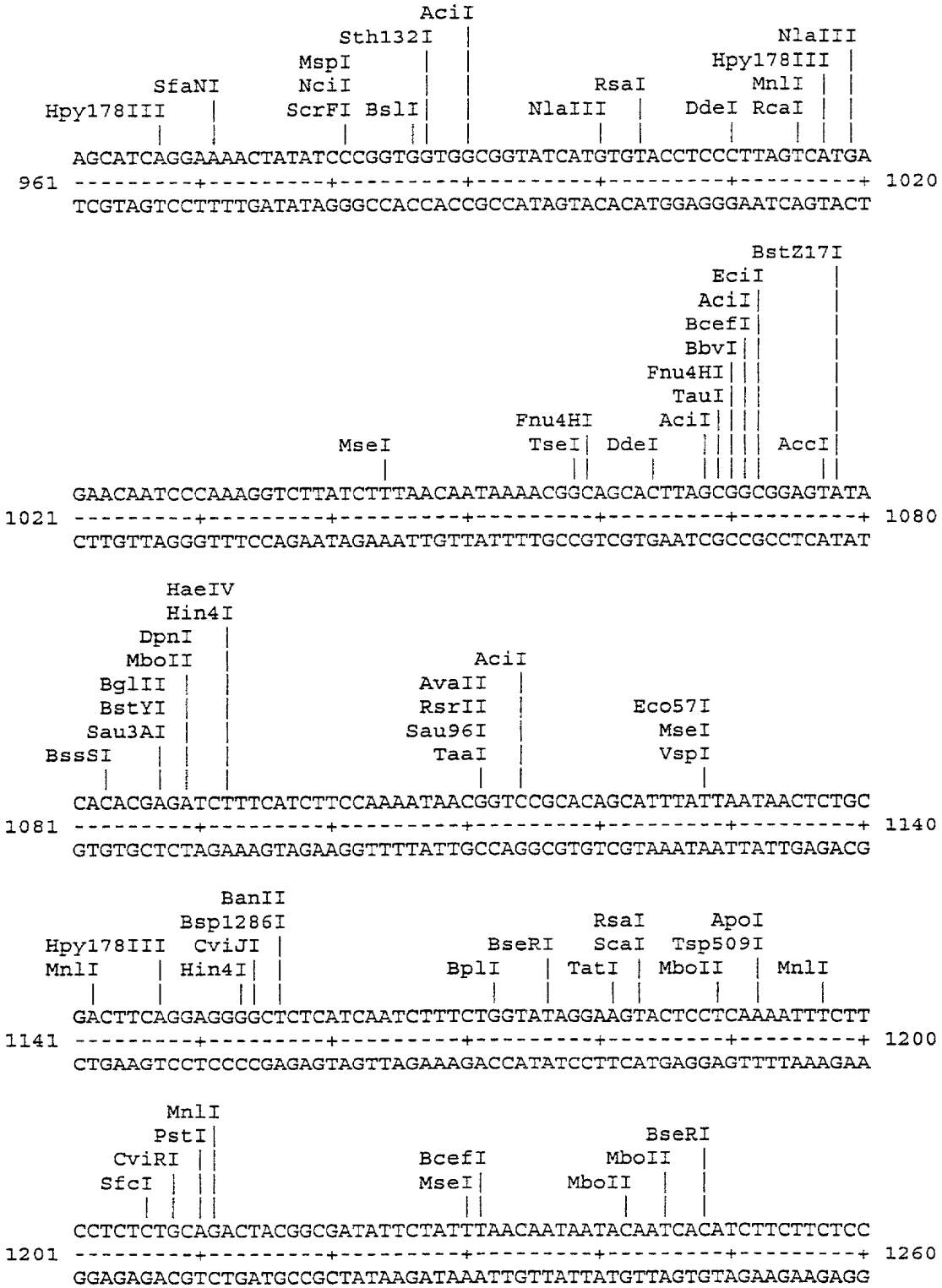

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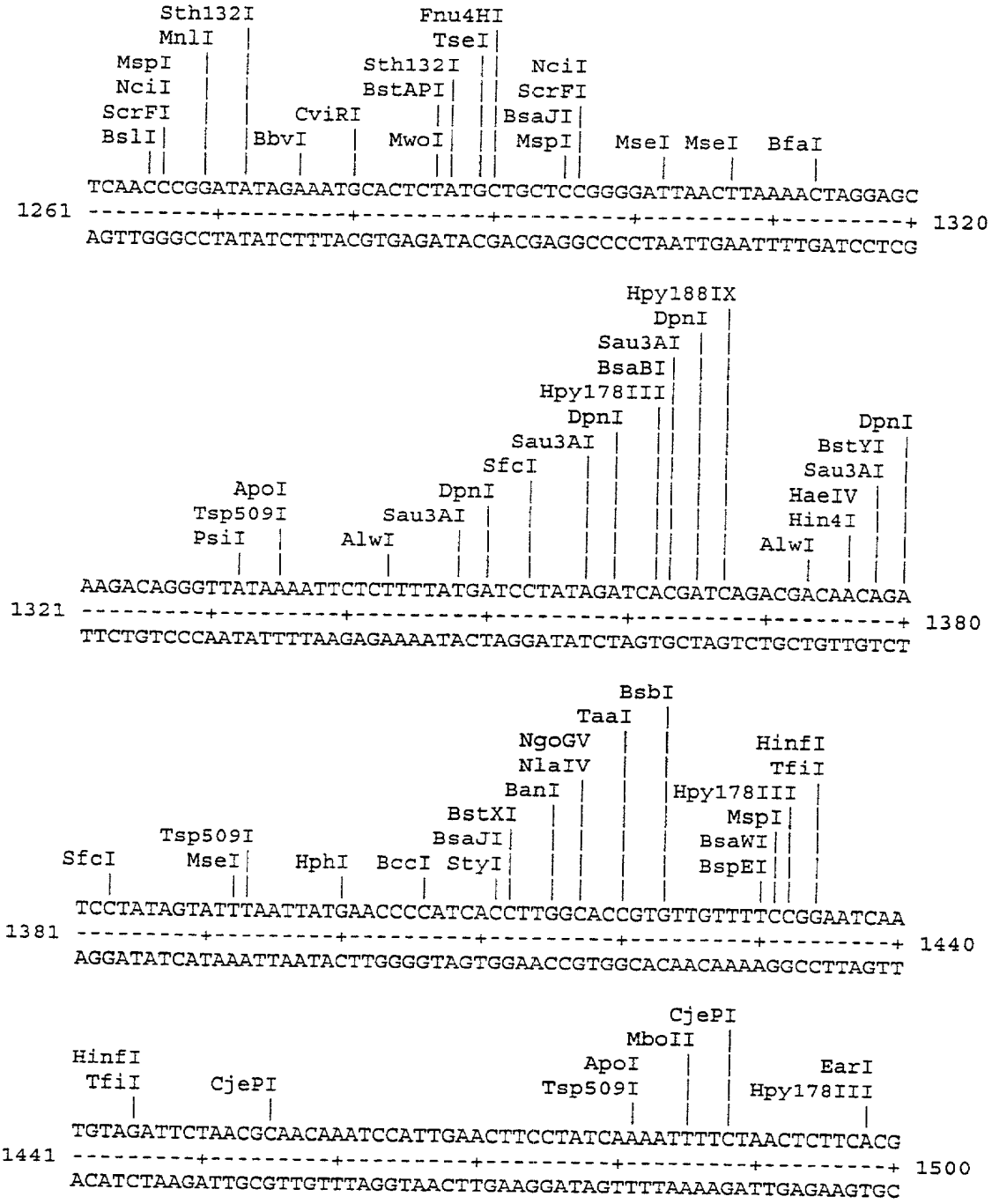

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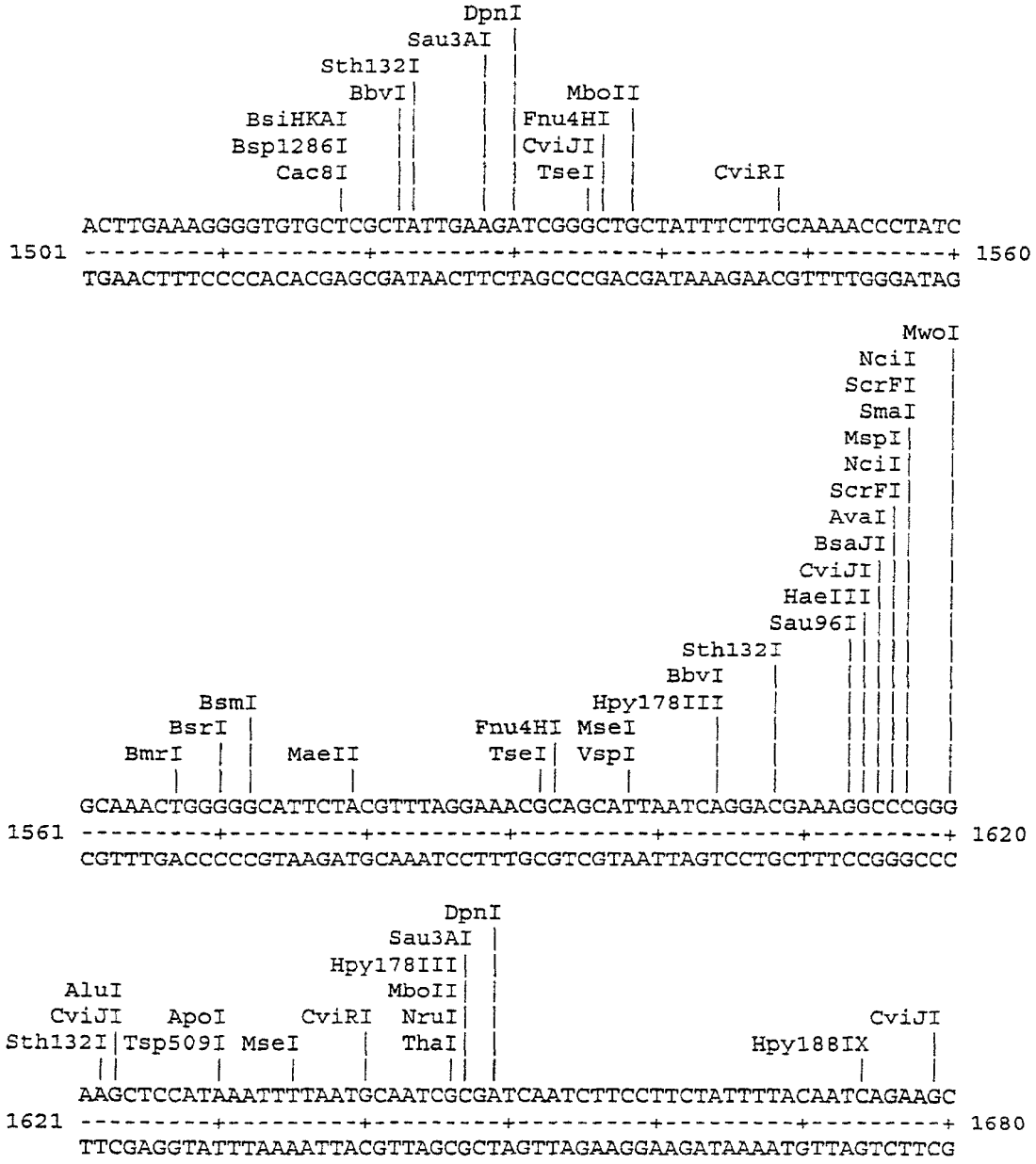

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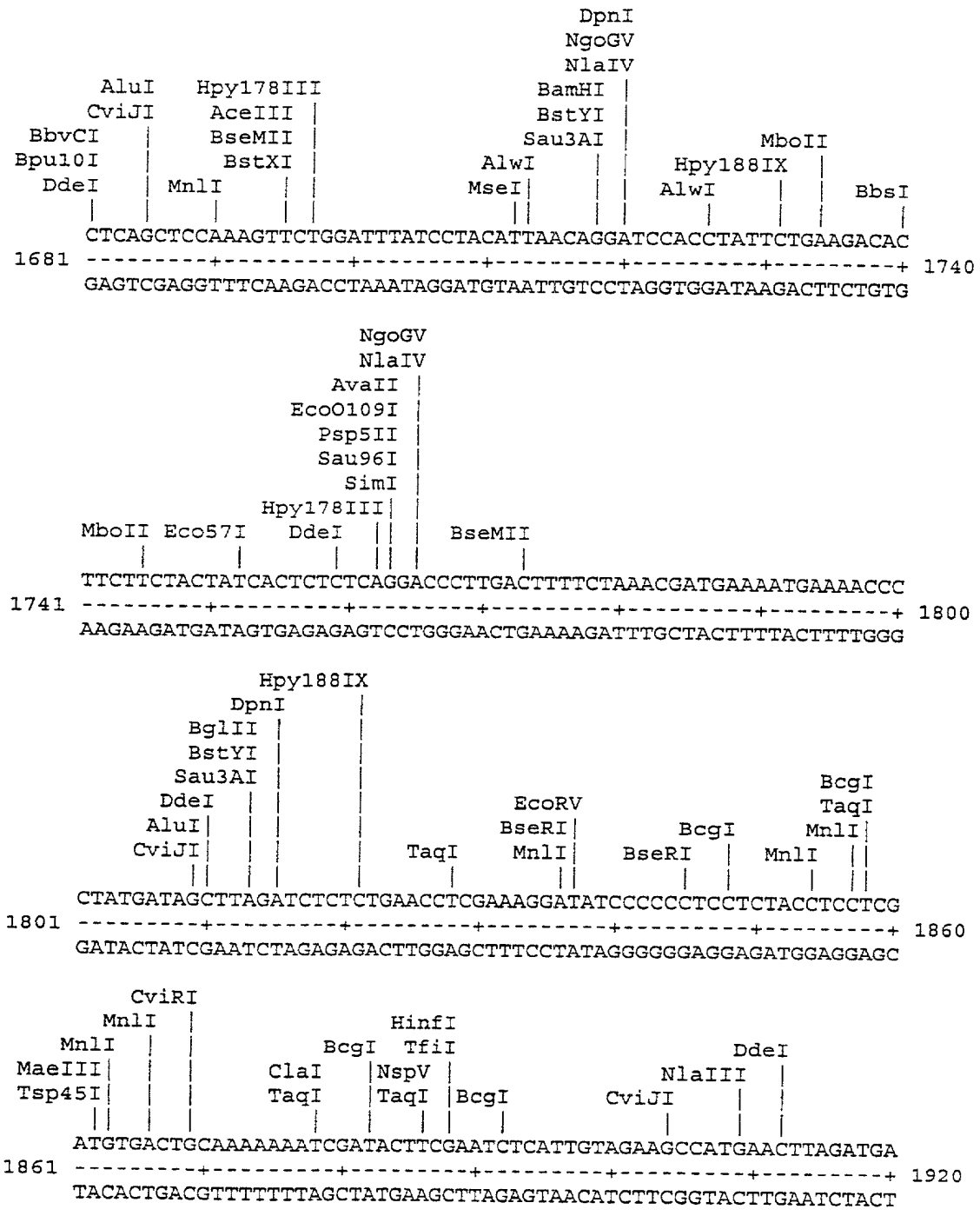

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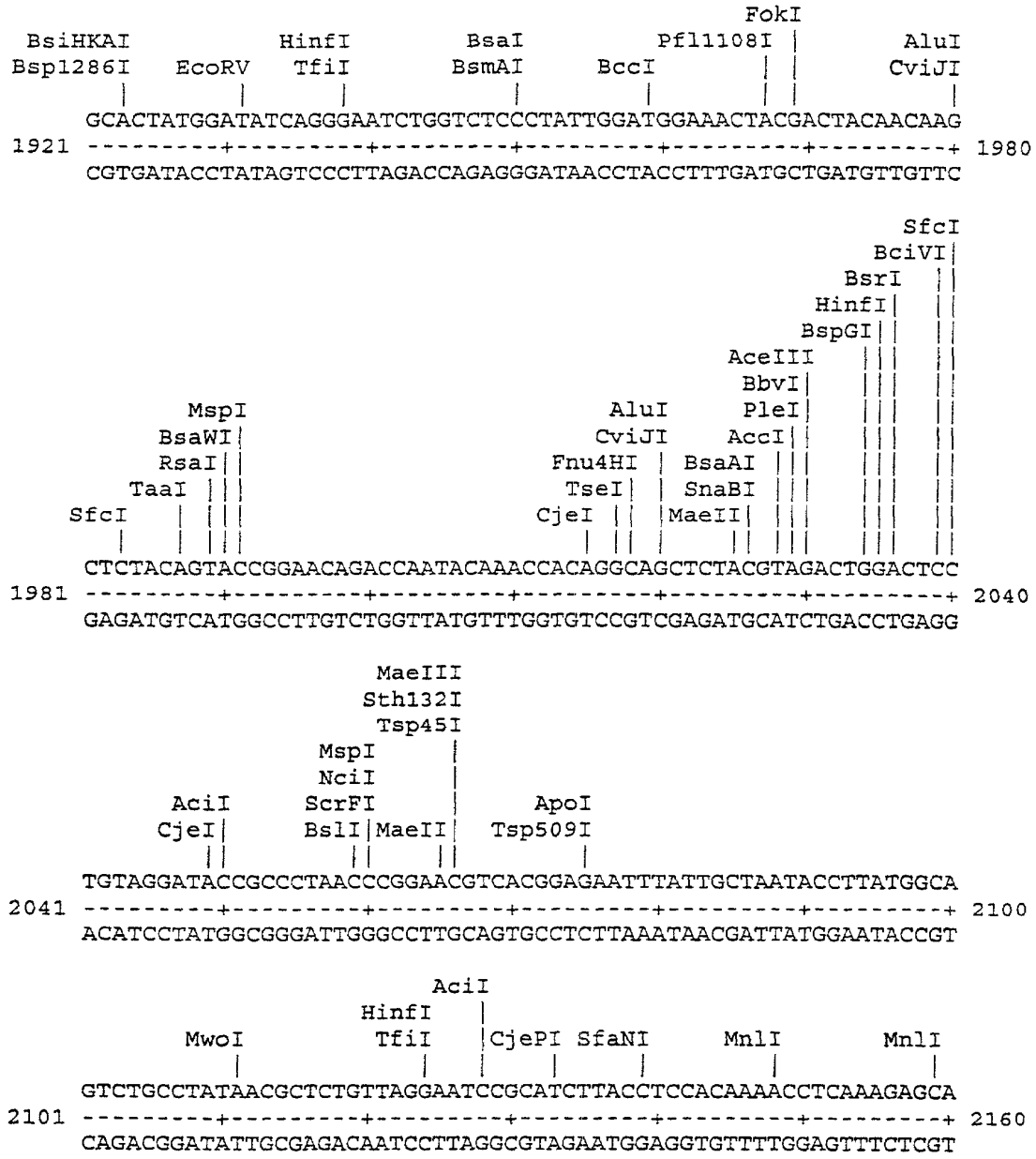

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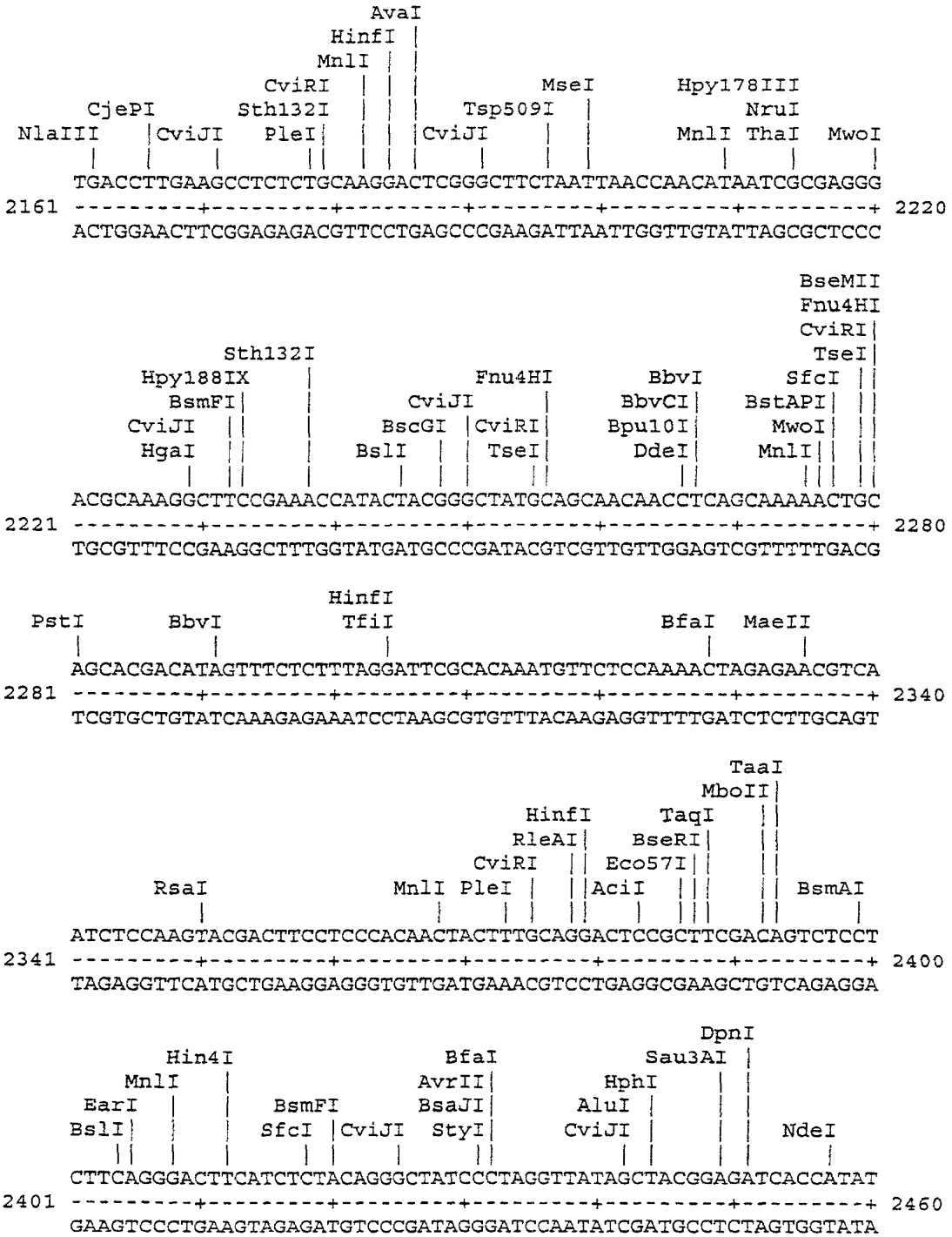

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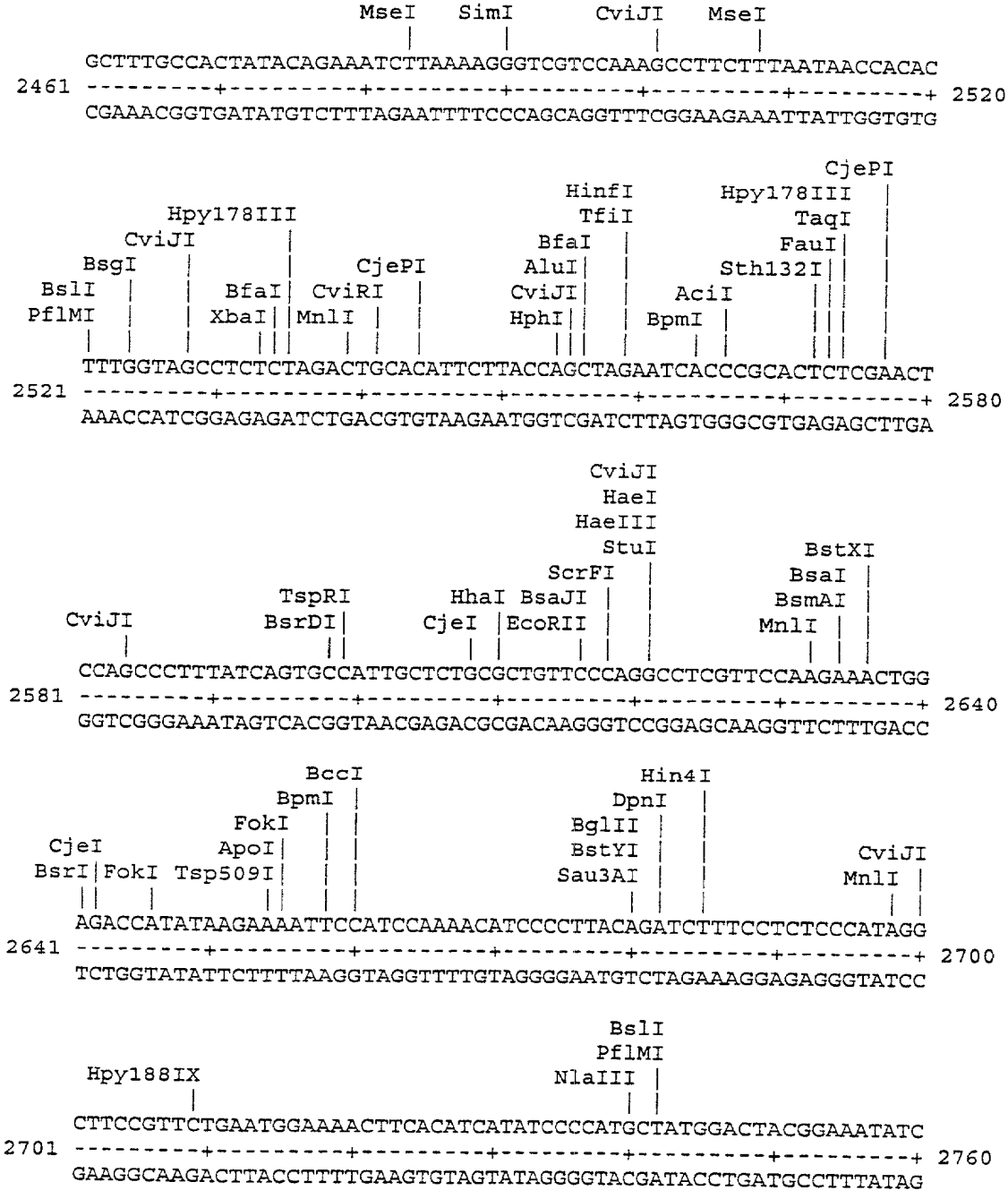

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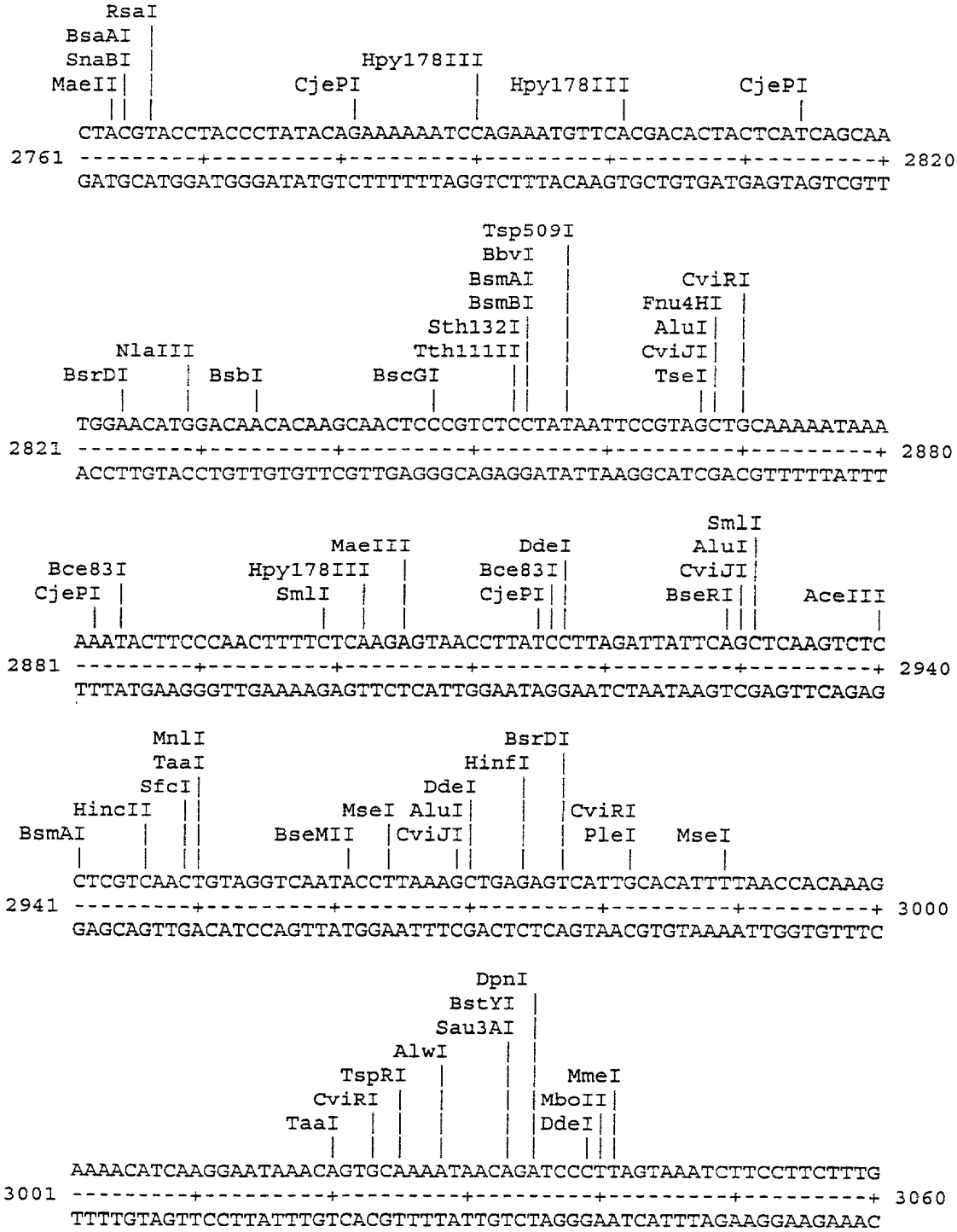

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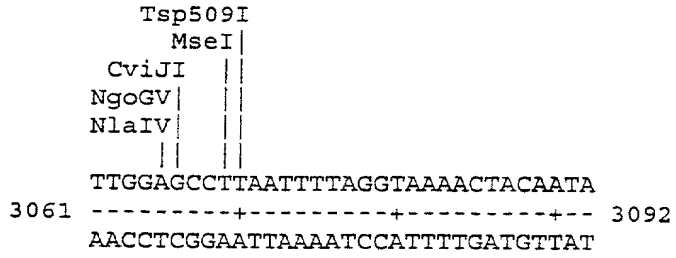


Figure 10

Restriction enzyme analysis of CPN100633 (RY 65 - SEQ ID NO. 10)

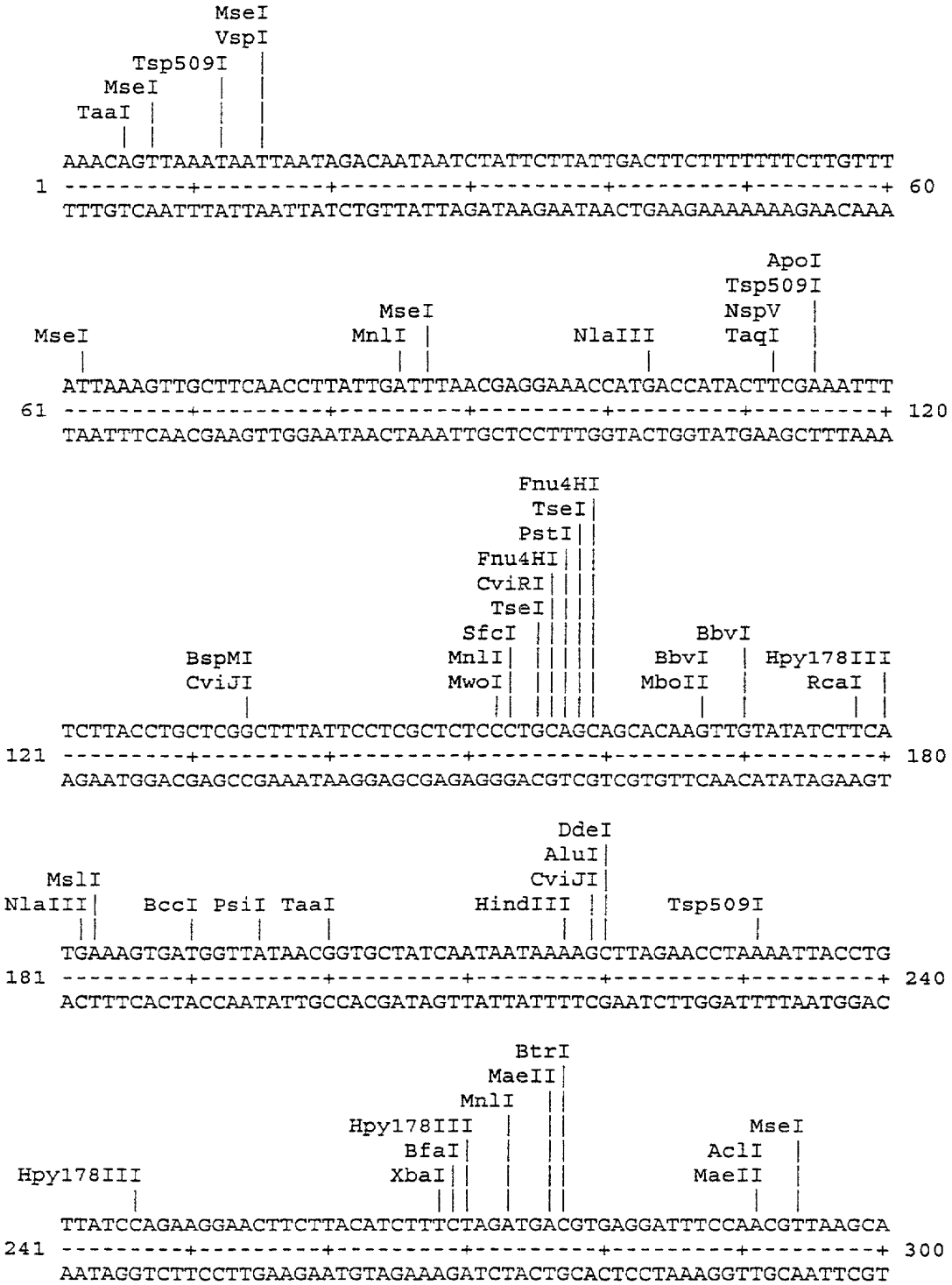


Figure 10 (continued)

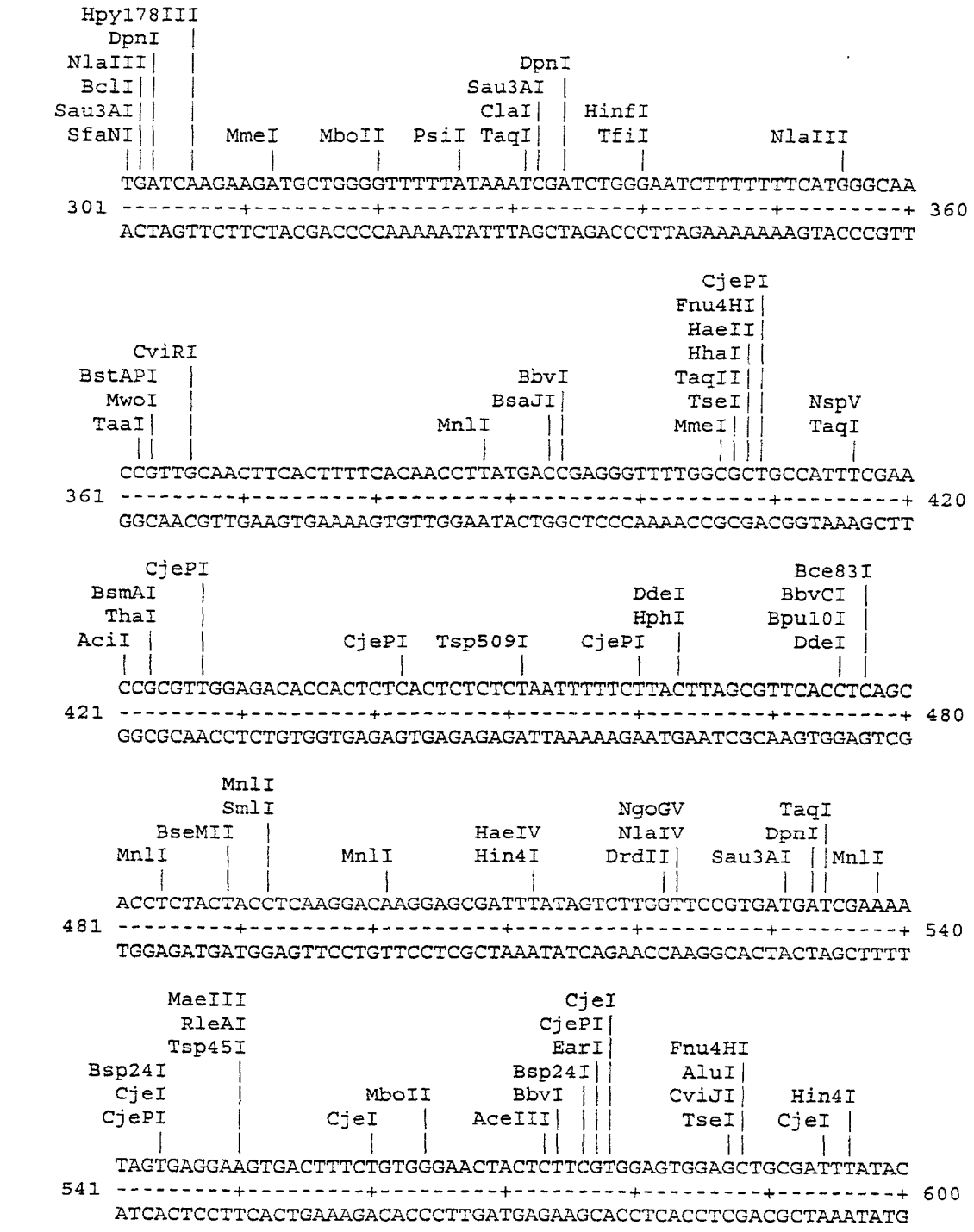
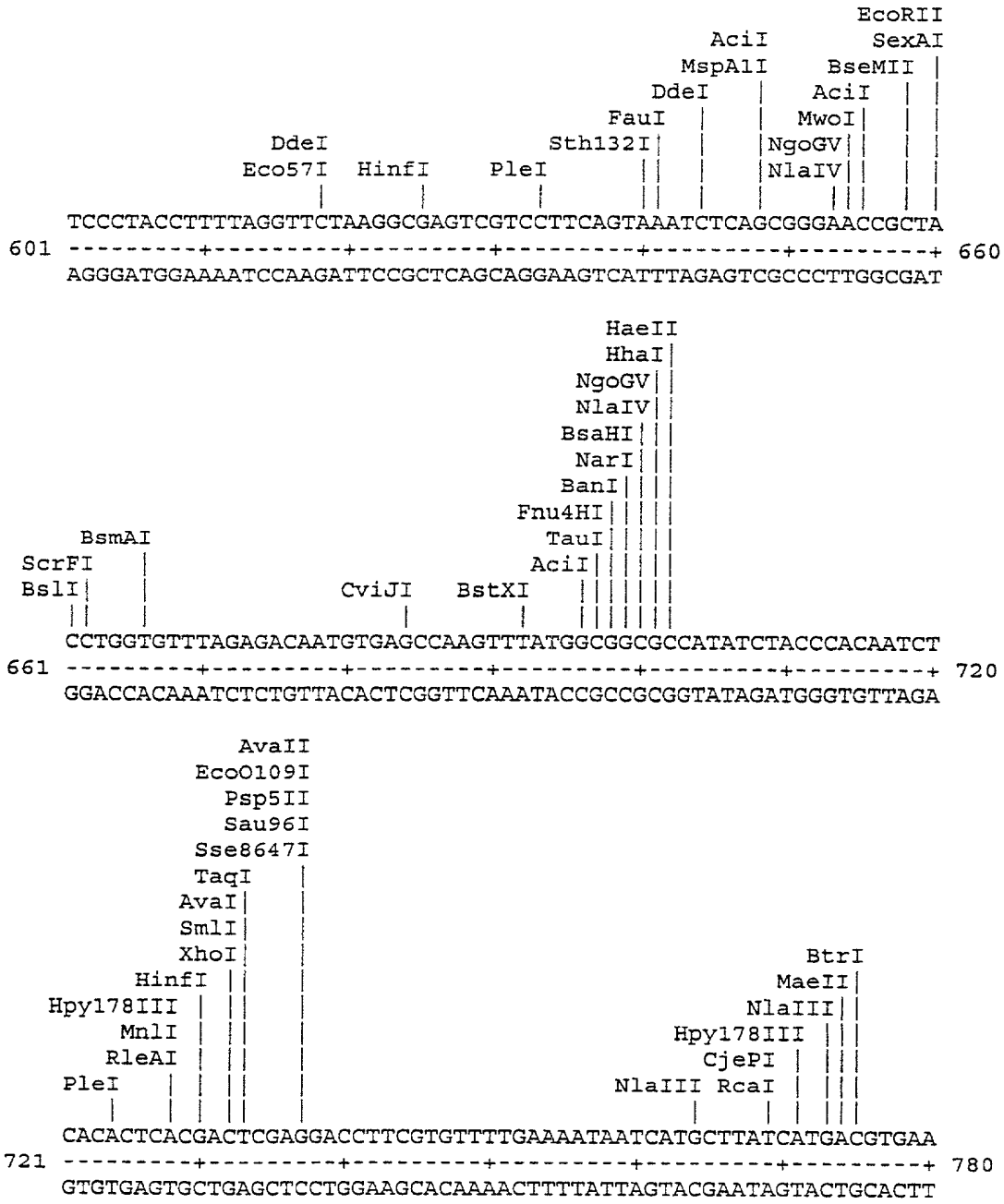


Figure 10 (continued)



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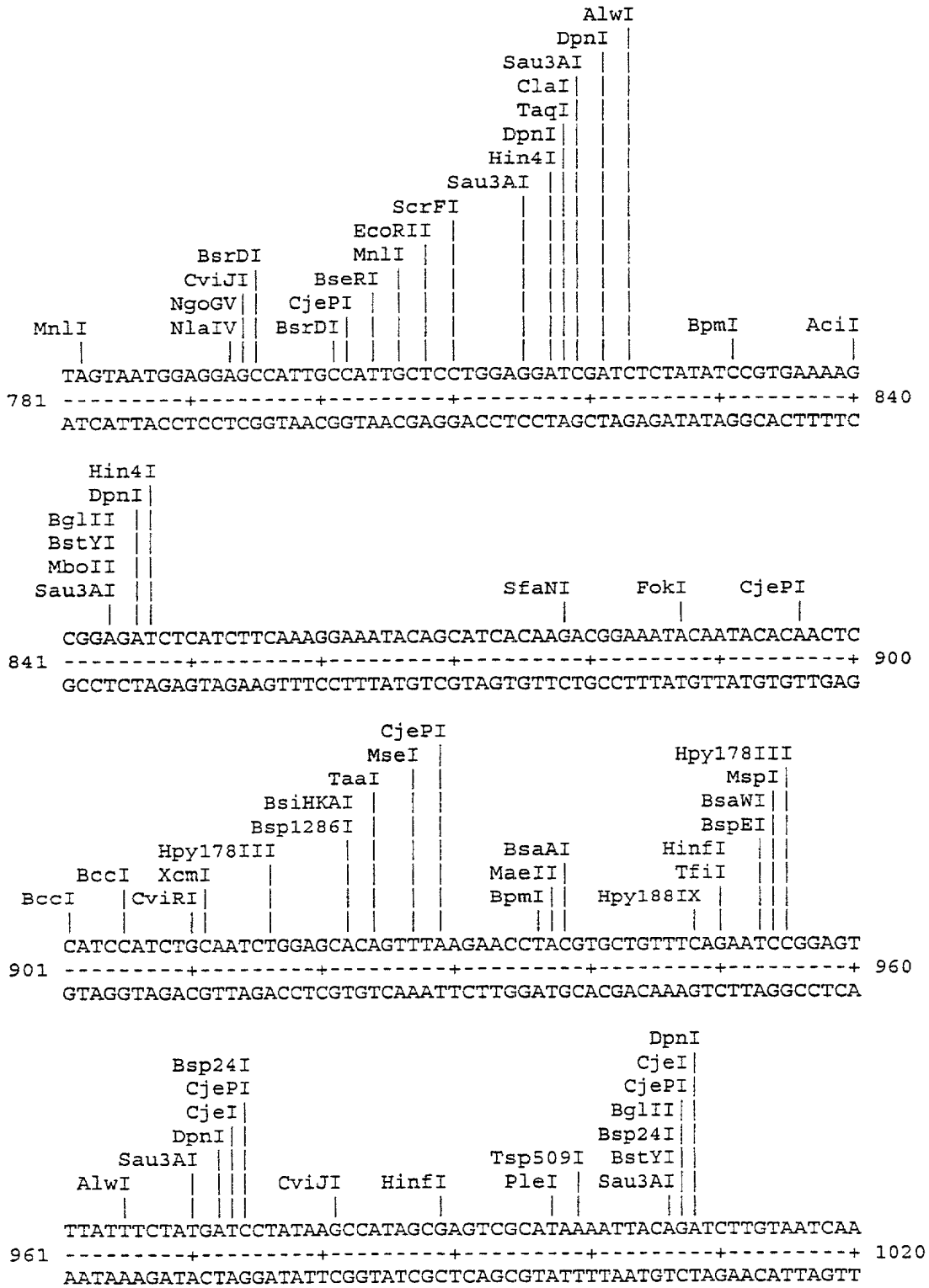

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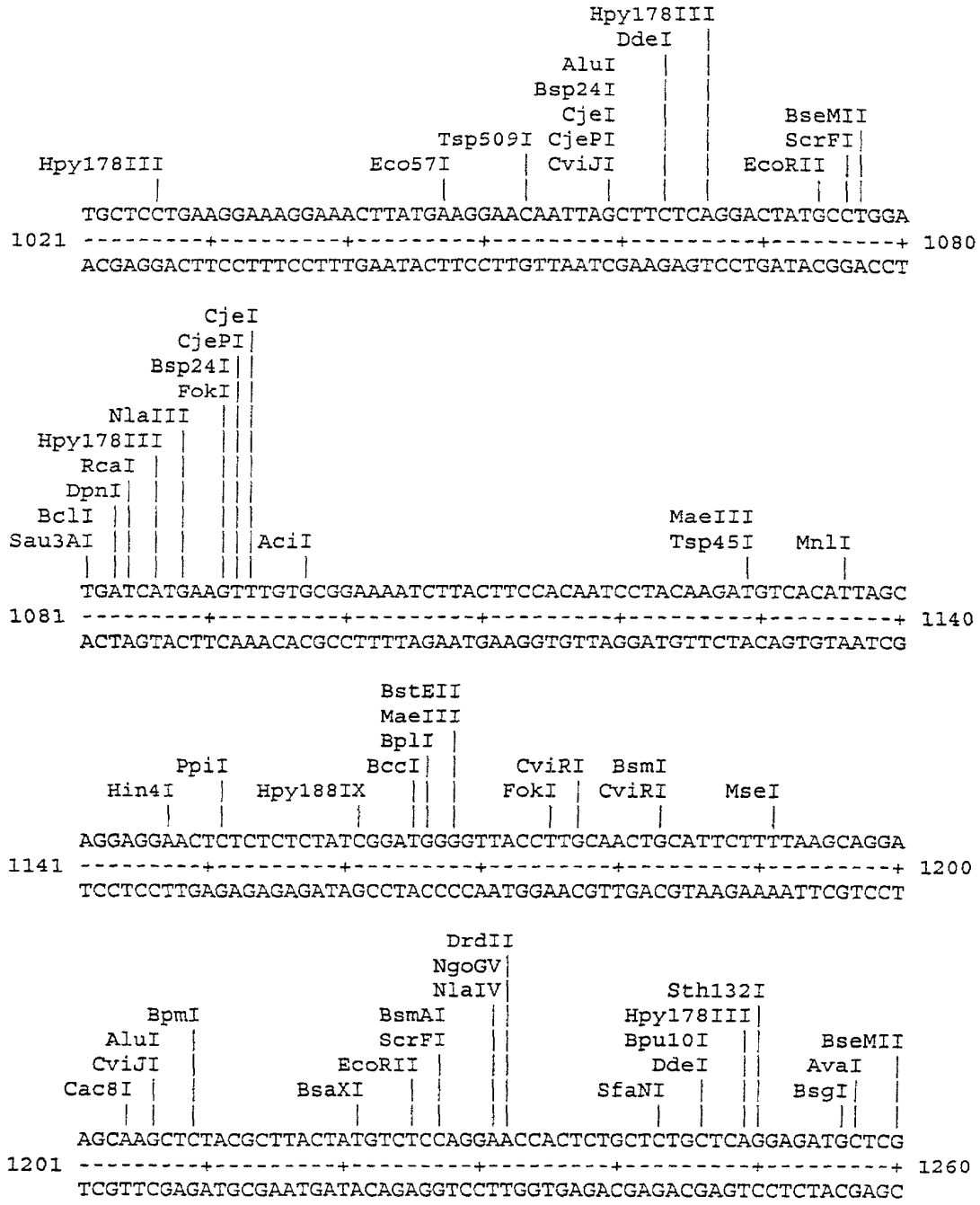

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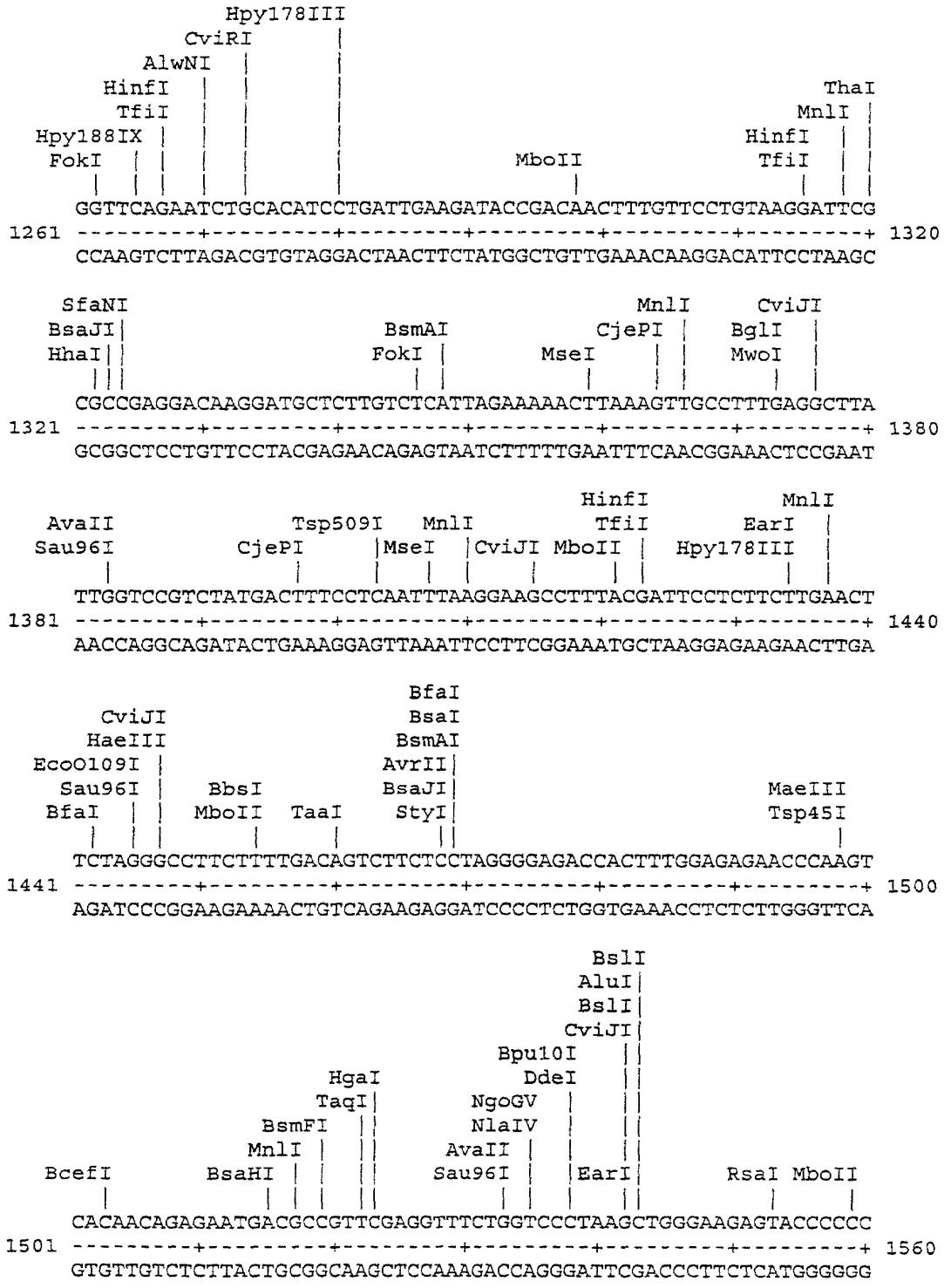
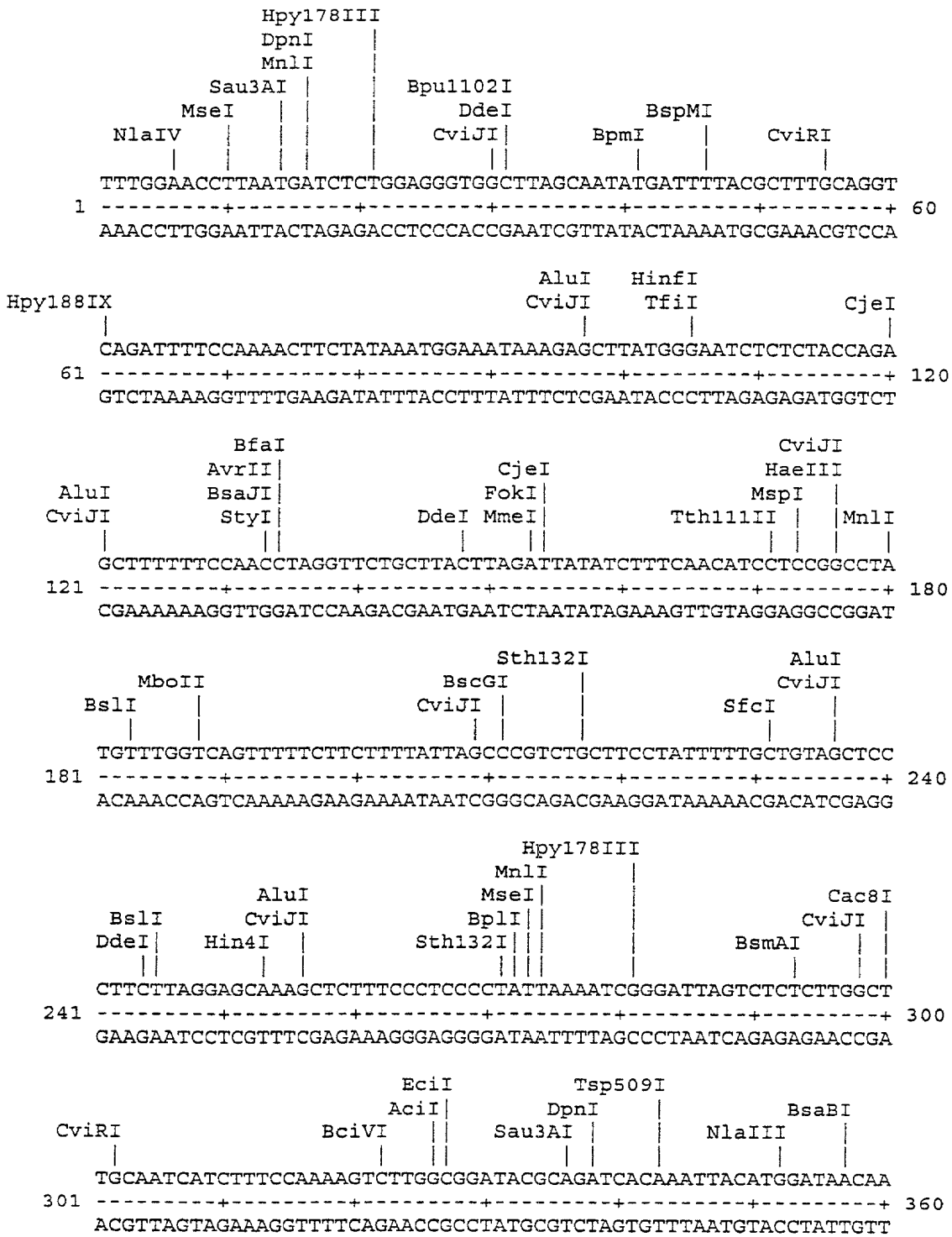


Figure 10 (continued)

Figure 11

Restriction enzyme analysis of CPN100985 (RY 66 - SEQ ID NO. 11)



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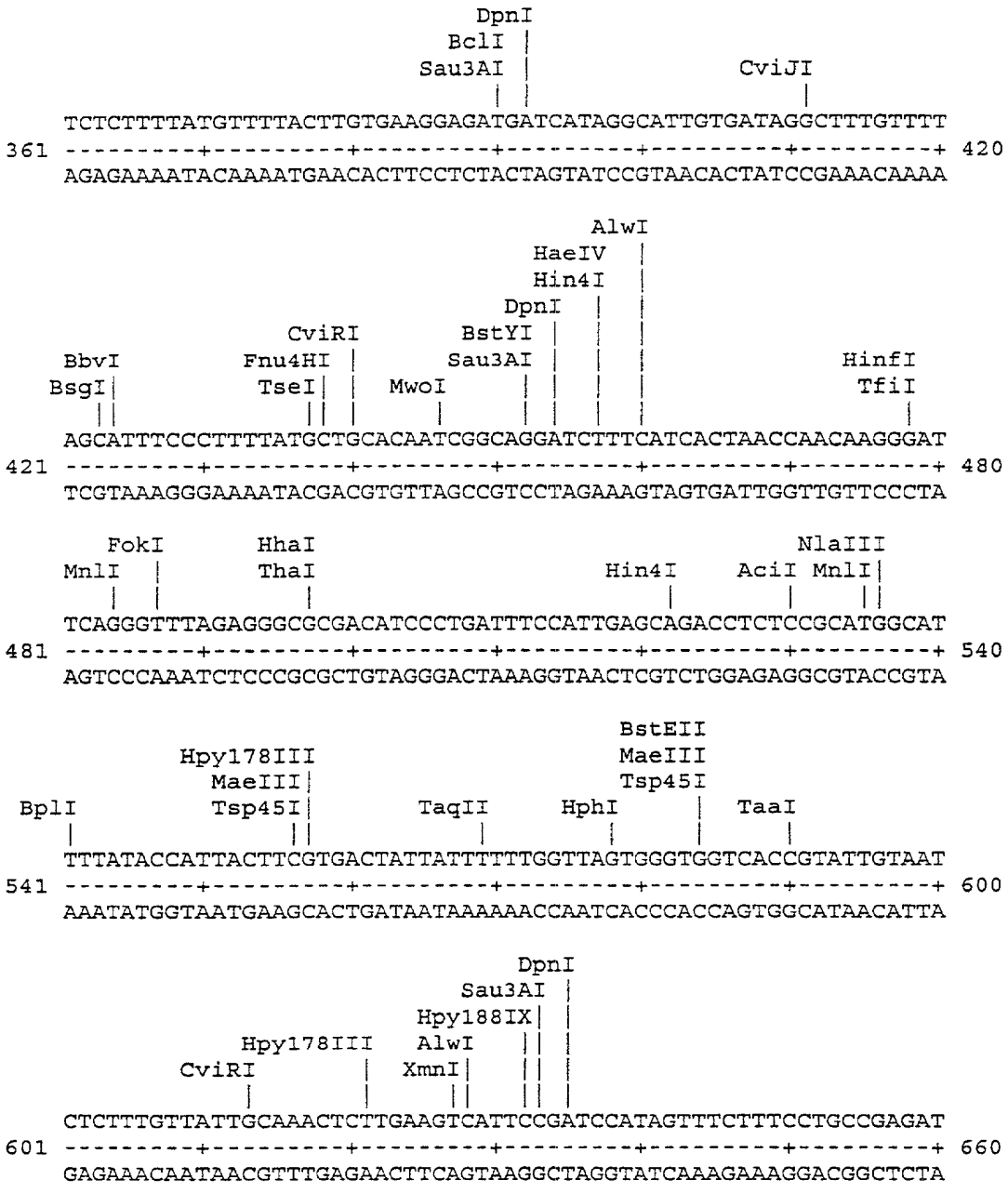

Figure 11 (continued)

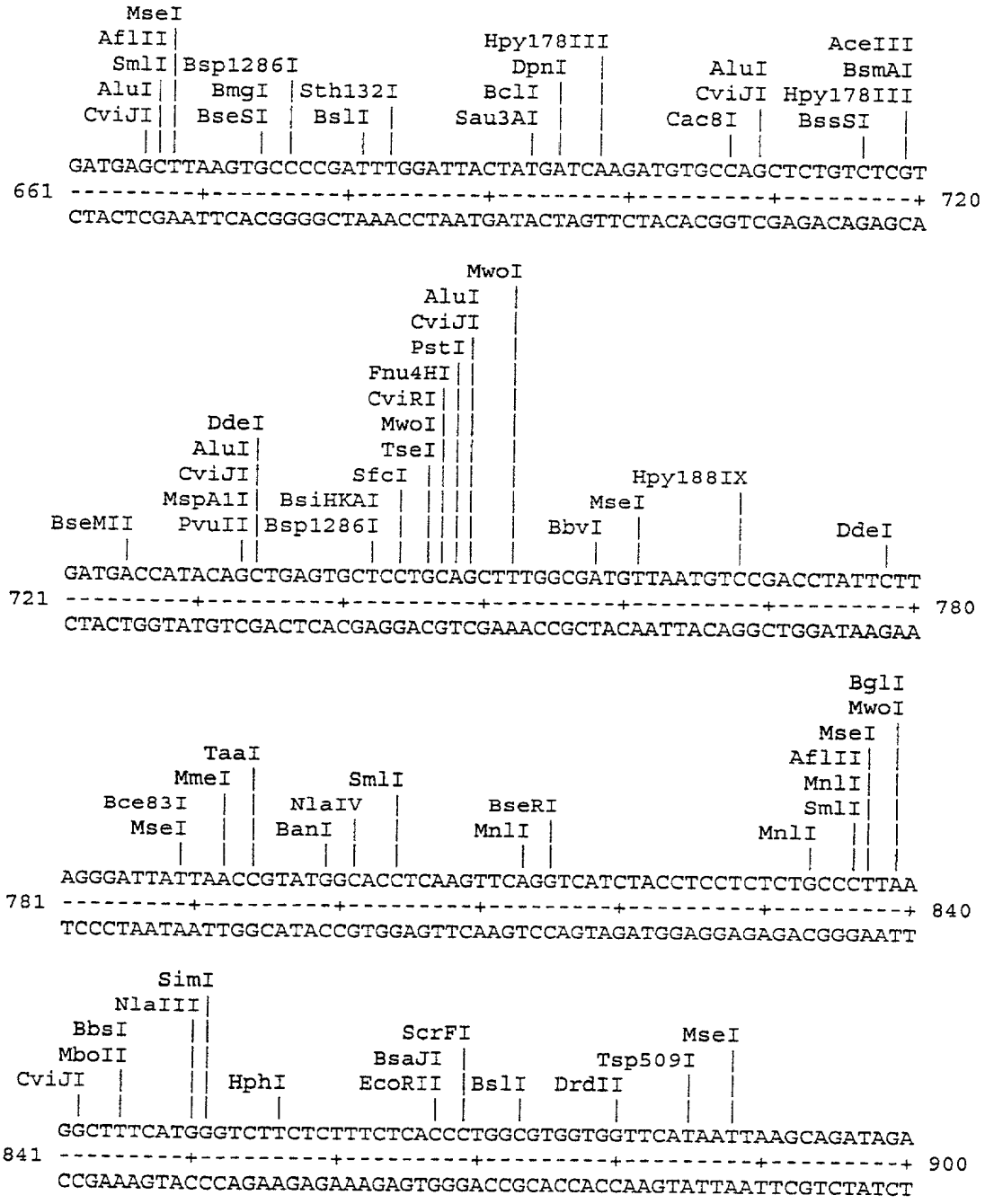

Figure 11 (continued)

```
                                                        BfaI
                                                      AvrII|
                                                      BsaJI|
                                 DrdII                 StyI|
   Tth111II        BsmFI           |                Bce83I||NlaIV       SmlI
        |              |         |                       |||    |          |
        TTATTTCACTCTTGCTTGGTTCAAAGAAGTCCCCATTATGCTCCTAGGTTCCAACCCTCA
   901 ---------+---------+---------+---------+---------+---------+ 960
        AATAAAGTGAGAACGAACCAAGTTTCTTCAGGGGTAATACGAGGATCCAAGGTTGGGAGT

                                               Hpy178III
                               CviJI         SfaNI    |
                            BfaI  |        HinfI   |    |
                  MnlI      MmeI  |Hpy178III |     |    |
               RsaI |     AvrII|  | MaeIII|  |     |    |
               ScaI |     BsaJI|  | Tsp45I|  |     |    |      HhaI        BpmI
             TatI | |      StyI|  | PleI  || |     |    | Hin4I  |      HinfI|
                | | |         ||  |    |  || |     |    |     |  |       TfiI|
                                                                          ||
        AGTACTCTAATCCCCTAGGCTCTTATCGTGACTCTTATCTGGAGATGCGCTCACTTACGA
   961 ---------+---------+---------+---------+---------+---------+ 1020
        TCATGAGATTAGGGGATCCGAGAATAGCACTGAGAATAGACCTCTACGCGAGTGAATGCT

                 BplI      TspRI              CjeI
               DdeI |    TaaI  |           HinfI |
             CjeI | |HhaI   |  |      DdeI  TfiI |                   DdeI
                | | |   |   |  |         |     | |                      |
        ATCTTAGCGCACTGTTTATGGATTATCTTAGGGAATCTCTCGCATATTCTTTTGTAATCT
  1021 ---------+---------+---------+---------+---------+---------+ 1080
        TAGAATCGCGTGACAAATACCTAATAGAATCCCTTAGAGAGCGTATAAGAAAACATTAGA

                     Hpy178III
            HinfI    ApoI    |
             TfiI Tsp509I    |
                |       |    |
        AAGAATCTATAAATTCAAGA
  1081 ---------+---------+ 1100
        TTCTTAGATATTTAAGTTCT
```

Figure 12

Restriction enzyme analysis of CPN100987 (RY 67 - SEQ ID NO. 12)

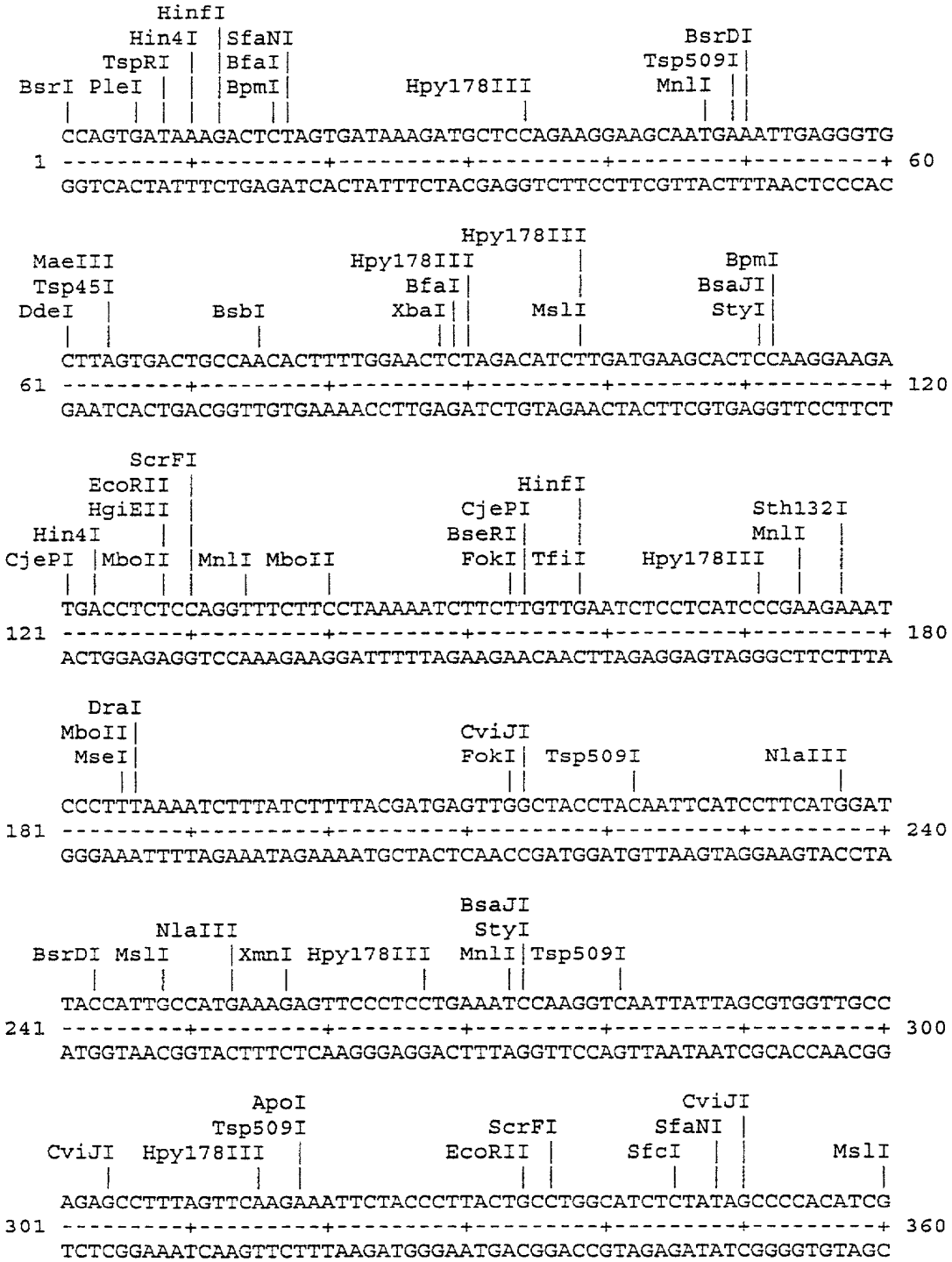

Figure 12 (continued)

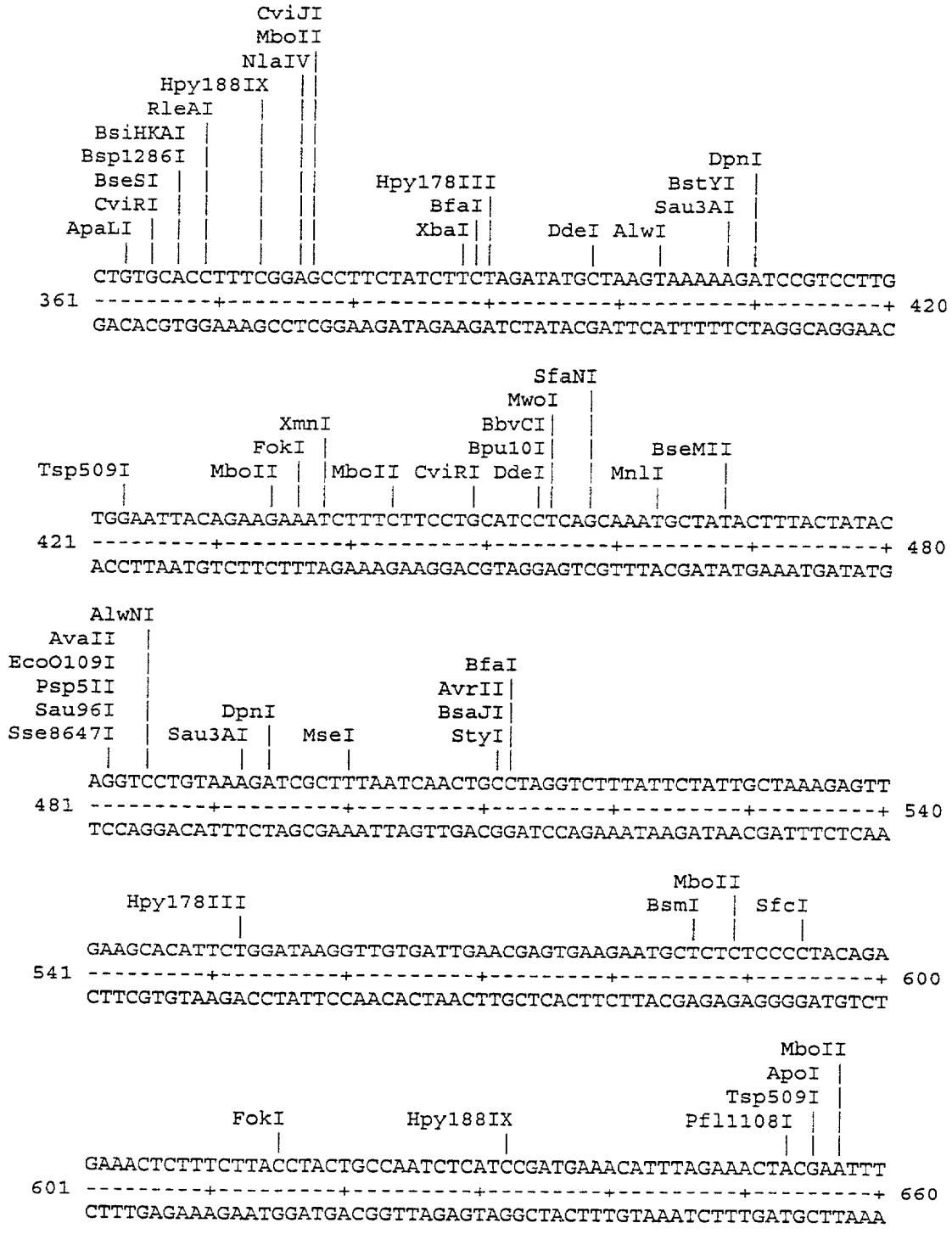

Figure 12 (continued)

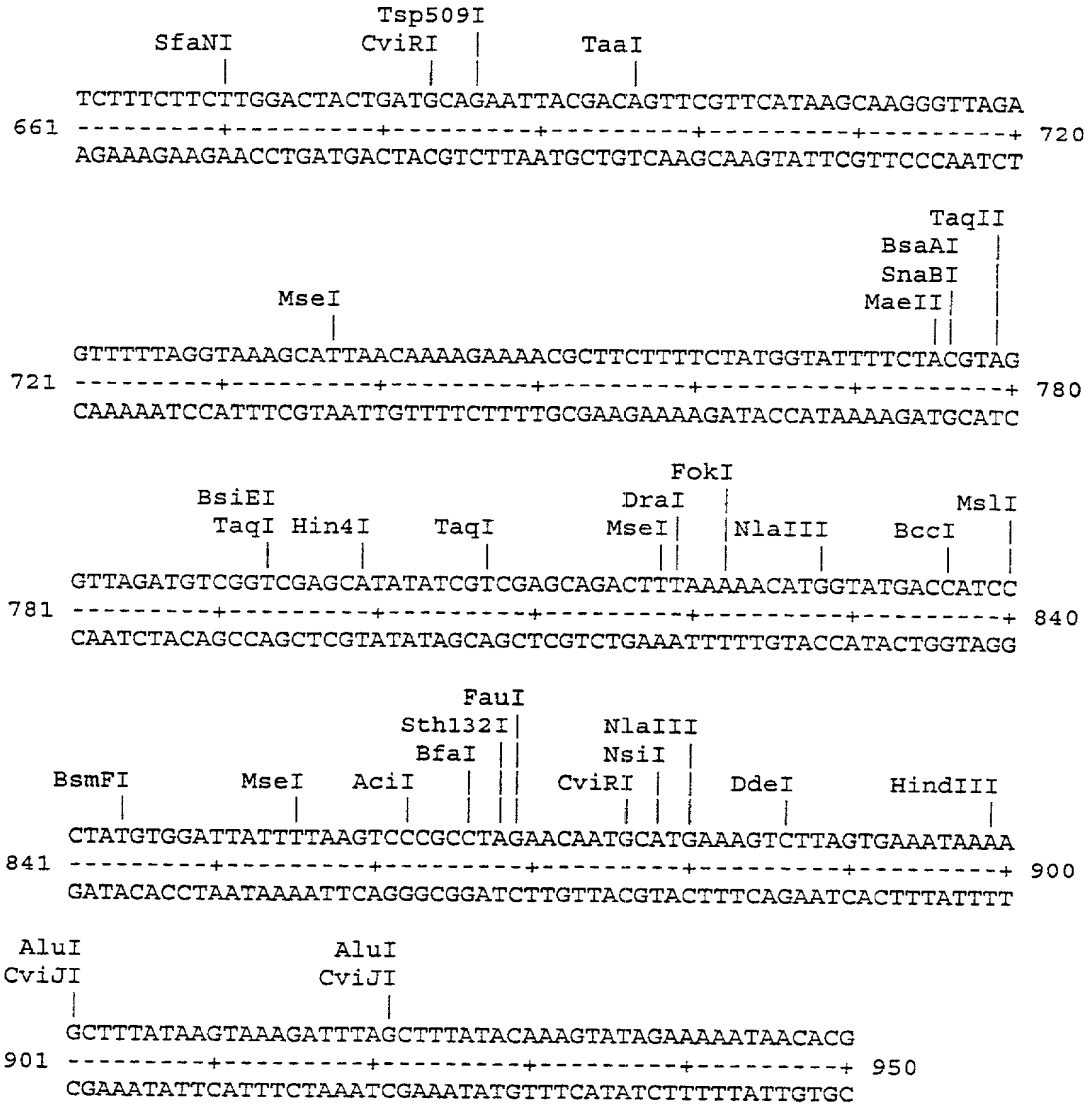

Figure 13

Restriction enzyme analysis of CPN100988 (ry68 - SEQ ID NO. 13)

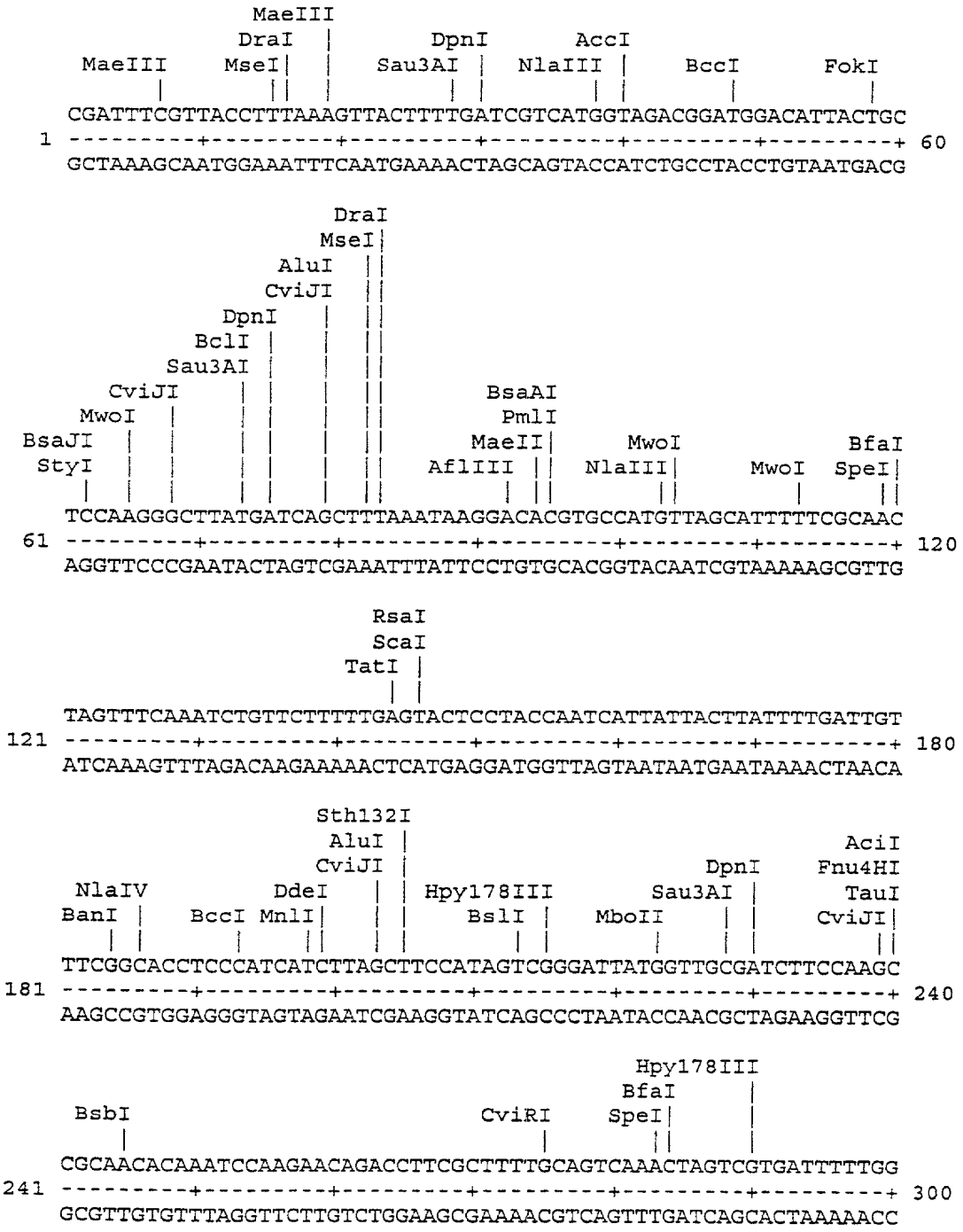

Figure 13 (continued)

```
                 Hpy178III
                 DpnI     |
                 MnlI     |
            Sau3AI |      |   Bpu1102I
         MseI   |  |      |       DdeI              BspMI          Hpy188IX
    NlaIV   |   |  |      |    CviJI|          BpmI     |      CviRI      |
        |   |   |  |      |         ||             |    |          |      |
        AACCTTAATGATCTCTGGAGGGTGGCTTAGCAATATGATTTTACGCTTTGCAGGTCAGAT
    301 ---------+---------+---------+---------+---------+---------+ 360
        TTGGAATTACTAGAGACCTCCCACCGAATCGTTATACTAAAATGCGAAACGTCCAGTCTA

                                                                  AluI
                                         AluI   HinfI            CviJI
                                        CviJI    TfiI            CjeI|
                                            |       |                ||
        TTTCCAAAACTTCTATAAATGGAAATAAAGAGCTTATGGGAATCTCTCTACCAGAGCTTT
    361 ---------+---------+---------+---------+---------+---------+ 420
        AAAGGTTTTGAAGATATTTACCTTTATTTCTCGAATACCCTTAGAGAGATGGTCTCGAAA

             BfaI                                        CviJI
            AvrII|                  CjeI                HaeIII
            BsaJI|                  FokI|              MspI   |    BslI
             StyI|          DdeI    MmeI|       Tth111II |    |MnlI  |
                ||             |      ||               |   |  |   |  |
        TTTCCAACCTAGGTTCTGCTTACTTAGATTATATCTTTCAACATCCTCCGGCCTATGTTT
    421 ---------+---------+---------+---------+---------+---------+ 480
        AAAGGTTGGATCCAAGACGAATGAATCTAATATAGAAAGTTGTAGGAGGCCGGATACAAA

     MboII
        |
        GGTCAGTTTTTCTTCTTTTA
    481 ---------+---------+ 500
        CCAGTCAAAAAGAAGAAAAT
```

Figure 14: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 14; ORF: cpn100686

```
  1 MVSSPILNVP LKNHASVSGK FTHREVSKLA SDLKSGAMSF VPEVLSEETI
 51 SSDLGKKQCT QGIISACCGL AMLIVLMSVY YRFGGVIASG AVLLNLLLIW
101 AALQYLDAPL TLSGLAGIVL AMGMAVDANV LVFERIREEF LLSQSLKKSV
151 EKGYTKAFGA IFDSNLTTVL ASALLFFLDT GPIKGFALTL ILGIFSSMFT
201 ALFMTKFFFM LWMNKTQHTQ LHMMNKFVGI KHDFLRGCKK LWAVSGSVFL
251 LGCVALGFGA WNSVLGMDFK GGYAFTFNPK EHGISDVAQM RGKVVHKLQE
301 AGLSSRDFRI QTFGSSEKIK IYFSDKALSY TKQIRASLLK LTIMSWRYCG
351 IVVRNRPRFL YGNSKRNAKF WSKVSSKLSK KMRYQATIGL LGALAIILLY
401 VSLRFEWQYA FSAVCALIHD LLATCAVLFI AHFFLKKIQI DLQAIGALMT
451 VLGYSLNNTL IIFDRIREDR QANLFTPMHV LVNDALQKTF SRTVMTTATT
501 LSVLLMLLFI GGSSVFNFAF IMTIGILLGT LSSLYIAPPL LLFMVRKENR
551 SK
```

Possible T cell epitope:

427 VLFIAHFFL

Possible B cell epitope:

465 RIREDRQAN

Figure 15: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 15; ORF: cpn100696

```
  1 MSSNLHPVGG TGTGAAAPES VLNIVEEIAA SGSVTAGLQA ITSSPGMVNL
 51 LIGWAKTKFI QPIRESKLFQ SRACQITLLV LGILLVVAGL ACMFIFHSQL
101 GANAFWLIIP AAIGLIKLLV TSLCFDEACT SEKLMVFQKW AGVLEDQLDD
151 GILNNSNKIF GHVKTEGNTS RATTPVLNDG RGTPVLSPLV SKIARV
```

Possible T cell epitope:

133 KLMVFQKWA

Possible B cell epitope:

163: VKTEGNTSRAT

Figure 16: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 16; ORF: cpn100709

```
  1 MTIRILAEGL AFRYGSKGPN IIHDVSFSVY DGDFIGIIGP NGGGKSTLTM
 51 LILGLLTPTF GSLKTFPSHS AGKQTHSMIG WVPQHFSYDP CFPISVKDVV
101 LSGRLSQLSW HGKYKKKDFE AVDHALDLVG LSDTTTTAFA HLSGGQIQRV
151 LLARALASYP EILILDEPTT NIDPDNQQRI LSILKKLNRT CTILMVTHDL
201 HHTTNYFNKV FYMNKTLHFI GRHFDLNRPI LLSSYKNQEF SCSPH
```

Possible T cell epitope:

212 YMNKTLHFI

Possible B cell epitopes:

109 SWHGKYKKKDFE

166 DEPTTNIDPDNQQR

Figure 17: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 17; ORF: cpn100710

```
  1 MHKVIVFIFL TLYSLKSYGN DVIDKPHVLV SIAPYKFLVE QIAEETCFVY
 51 AIVTNHYDPH TYELPPQQIK ELRQGDLWFR IGEAFGKNLL EKPYMQQVDL
101 SQNVSLIQGK PCCNQHTTNY DTHTWLSPKN LKVQVETIVT TLSKKYPQHA
151 TLYQSNGEKL LLALDQLNEE ILTITSKAKQ RHILVSHGAF GYFCRDYNFS
201 QHTIEKSSHV EPSPKDVARV FRDIEQYKIS SVILLEYSGR RSSAMLADRF
251 HMHTVNLDPY AENVLVNLKT IATTFSSL
```

Possible T cell epitope:

125 WLSPKNLKV

Possible B cell epitope:

55 NHYDPHTYELPPQQIKELRQGD

Figure 18: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 18; ORF: cpn100711

```
  1 MGPGSVLSNH SKEAGGIAIN NVIIDFSEIV PTKDNATVAP PTLKLVSRTN
 51 ADSKDKIDIT GTVTLLDPNG NLYQNSYLGE DRDITLFNID NSASGAVTAT
101 NVTLQGNLGA KKGYLGTWNL DPNSSGSKII LKWTFDKYLR WPYIPRDNHF
151 YINSIWGAQN SLVTVNQGIL GNMLNNARFE DPAFNNFWAS AIGSFLRKEV
201 SRNSDSFTYH GRGYTAAVDA KPRQEFILGA AFSQVFGHAE SEYHLDNYKH
251 KGSGHSTQAS LYAGNIFYFP AIRSRPILFQ GVATYGYMQH DTTTYYPSIE
301 EKNMANWDSI AWLFDLRFSV DLKEPQPHST ARLTFYTEAE YTRIRQEKFT
351 ELDYDPRSFS ACSYGNLAIP TGFSVDGALA WREIILYNKV SAAYLPVILR
401 NNPKATYEVL STKEKGNVVN VLPTRNAARA EVSSQIYLGS YWTLYGTYTI
451 DASMNTLVQM ANGGIRFVF
```

Possible T cell epitope:

312 WLFDLRFSV

Possible B cell epitope:

240: ESEYHLDNYKHKGSGHST

Figure 19: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 19; ORF: cpn100877

```
  1 MRFSLCGFPL VFSFTLLSVF DTSLSATTIS LTPEDSFHGD SQNAERSYNV
 51 QAGDVYSLTG DVSISNVDNS ALNKACFNVT SGSVTFAGNH HGLYFNNISS
101 GTTKEGAVLC CQDPQATARF SGFSTLSFIQ SPGDIKEQGC LYSKNALMLL
151 NNYVVRFEQN QSKTKGGAIS GANVTIVGNY DSVSFYQNAA TFGGAIHSSG
201 PLQIAVNQAE IRFAQNTAKN GSGGALYSDG DIDIDQNAYV LFRENEALTT
251 AIGKGGAVCC LPTSGSSTPV PIVTFSDNKQ LVFERNHSIM GGGAIYARKL
301 SISSGGPTLF INNISYANSQ NLGGAIAIDT GGEISLSAEK GTITFQGNRT
351 SLPFLNGIHL LQNAKFLKLQ ARNGYSIEFY DPITSEADGS TQLNINGDPK
401 NKEYTGTILF SGEKSLANDP RDFKSTIPQN VNLSAGYLVI KEGAEVTVSK
451 FTQSPGSHLV LDLGTKLIAS KEDIAITGLA IDIDSLSSSS TAAVIKANTA
501 NKQISVTDSI ELISPTGNAY EDLRMRNSQT FPLLSLEPGA GGSVTVTAGD
551 FLPVSPHYGF QGNWKLAWTG TGNKVGEFFW DKINYKPRPE KEGNLVPNIL
601 WGNAVDVRSL MQVQETHASS LQTDRGLWID GIGNFFHVSA SEDNIRYRHN
651 SGGYVLSVNN EITPKHYTSM AFSQLFSRDK DYAVSNNEYR MYLGSYLYQY
701 TTSLGNIFRY ASRNPNVNVG ILSRRFLQNP LMIFHFLCAY GHATNDMKTD
751 YANFPMVKNS WRNNCWAIEC GGSMPLLVFE NGRLFQGAIP FMKLQLVYAY
801 HGDFKETTAD GRRFSNGSLT SISVPLGIRF EKLALSQDVL YDFSFSYIPD
851 IFRKDPSCEA ALVISGDSWL VPAAHVSRHA FVGSGTGRYH FNDYTELLCR
901 GSIECRPHAR NYNINCGSKF RF
```

Possible T cell epitope:

146 ALMLLNNYV

Possible B cell epitope:

581 DKINYKPRPEKEG

Figure 20: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 20; ORF: CPN100325

```
  1 MPSSWKRLLQ VLSHKIAATE SGGGIYAKDI QLQALPGSFT ITDNKVETSL
 51 TTSTNLYGGG IYSSGAVTLT NISGTFGITG NSVINTATSQ DADIQGGGIY
101 ATTSLSINQC NTPILFSNNS AATKKTSTTK QIAGGAIFSA AVTIENNSQP
151 IIFLNNSAKS EATTAATAGN KDSCGGAIAA NSVTLTNNPE ITFKGNYAET
201 GGAIGCIDLT NGSPPRKVSI ADNGSVLFQD NSALNRGGAI YGETIDISRT
251 GATFIGNSSK HDGSAICCST ALTLAPNSQL IFENNKVTET TATTKASINN
301 LGAAIYGNNE TSDVTISLSA ENGSIFFKNN LCTATNKYCS IAGNVKFTAI
351 EASAGKAISF YDAVNVPPKK QLLKS
```

Possible T cell epitope:

226 VLFQDNSAL

Possible B cell epitope:

257 NSSKHDG

Figure 21: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 21; ORF: CPN100368

```
   1 MKYSLPWLLT SSALVFSLHP LMAANTDLSS SDNYENGSSG SAAFTAKETS
  51 DASGTTYTLT SDVSITNVSA ITPADKSCFT NTGGALSFVG ADHSLVLQTI
 101 ALTHDGAAIN NTNTALSFSG FSSLLIDSAP ATGTSGGKGA ICVTNTEGGT
 151 ATFTDNASVT LQKNTSEKDG AAVSAYSIDL AKTTTAALLD QNTSTKNGGA
 201 LCSTANTTVQ GNSGTVTFSS NTATDKGGGI YSKEKDSTLD ANTGVVTFKS
 251 NTAKTGGAWS SDDNLALTGN TQVLFQENKT TGSAAQANNP EGCGGAICCY
 301 LATATDKTGL AISQNQEMSF TSNTTTANGG AIYATKCTLD GNTTLTFDQN
 351 TATAGCGGAI YTETEDFSLK GSTGTVTFST NTAKTGGALY SKGNSSLTGN
 401 TNLLFSGNKA TGPSNSSANQ EGCGGAILAF IDSGSVSDKT GLSIANNQEV
 451 SLTSNAATVS GGAIYATKCT LTGNGSLTFD GNTAGTSGGA IYTETEDFTL
 501 TGSTGTVTFS TNTAKTGGAL YSKGNNSLSG NTNLLFSGNK ATGPSNSSAN
 551 QEGCGGAILS FLESASVSTK KGLWIEDNEN VSLSGNTATV SGGAIYATKC
 601 ALHGNTTLTF DGNTAETAGG AIYTETEDFT LTGSTGTVTF STNTAKTAGA
 651 LHTKGNTSFT KNKALVFSGN SATATATTTT DQEGCGGAIL CNISESDIAT
 701 KSLTLTENES LSFINNTAKR SGGGIYAPKC VISGSESINF DGNTAETSGG
 751 AIYSKNLSIT ANGPVSFTNN SGGKGGAIYI ADSGELSLEA IDGDITFSGN
 801 RATEGTSTPN SIHLGARGKI TKLAAAPGHT IYFYDPITME APASGGTIEE
 851 LVINPVVKAI VPPPQPKNGP I
```

Possible T cell epitope:

7	WLLTSSALV

Possible B cell epitopes:

162	QKNTSEKDG
538	GNKATGPSNSSANQEG

Figure 22: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 22; ORF: CPN100624

```
  1 MTNSIFISKF GCLCDPFVSA FYPTALCCSL SGNEVPNLAS CQMSRKDISA
 51 FHTSPSFRLN VTPEPLVSSF RPSNLLNGFG HDITQDITIT GNSINSVIDY
101 NYHYEDGGIL ACKNLFISEN KGNLSFERNS SHSSGGALYS VRECWISKNQ
151 NYSFISNAAS LATTTTSGFG GAIHALDSYI TNNLGEGQFL DNVSKNRGGA
201 IYVGVSLSIT DNLGPIVIKK NQTLEDSSFG GGIFCRAVNI ERNYQNIQIN
251 DNASGQGVVY FLPLGVIISS NKEIIEISNH SASSINTASG KLYPGGGGIM
301 CTSLSHENNP KGLIFNNKTA ALSGGVYTRD LSSSKITVRT AFINNSATSG
351 GALINLSGIG STPQNFFLSA DYGDILFNNN TITSSSPQPG YRNALYAAPG
401 INLKLGARQG YKILFYDPID HDQTTTDPIV FNYEPHHLGT VLFSGINVDS
451 NATNPLNFLS KFSNSSRLER GVLAIEDRAA ISCKTLSQTG GILRLGNAAL
501 IRTKGPGSSI NFNAIAINLP SILQSEASAP KFWIYPTLTG STYSEDTSST
551 ITLSGPLTFL NDENENPYDS LDLSEPRKDI PPPLPPRCDC KKIDTSNLIV
601 EAMNLDEHYG YQGIWSPYWM ETTTTTSSTV PEQTNTNHRQ LYVDWTPVGY
651 RPNPERHGEF IANTLWQSAY NALLGIRILP PQNLKEHDLE ASLQGLGLLI
701 NQHNREGRKG FRNHTTGYAA TTSAKTAARH SFSLGFAQMF SKTRERQSPS
751 TTSSHNYFAG LRFDSLLFRD FISTGLSLGY SYGDHHMLCH YTEILKGSSK
801 AFFNNHTLVA SLDCTFLPAR ITRTLELQPF ISAIALRCSQ ASFQETGDHI
851 RKFHPKHPLT DLSSPIGFRS EWKTSHHIPM LWTTEISYVP TLYRKNPEMF
901 TTLLISNGTW TTQATPVSYN SVAAKIKNTS QLFSRVTLSL DYSAQVSSST
951 VGQYLKAESH CTF
```

Possible T cell epitope:

640 QLYVDWTPV

Possible B cell epitopes:

701 NQHNREGRKGFRNHTTG

741 SKTRERQSPSTTSSHNY

Figure 23: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 23; ORF: CPN100633

```
  1 MTILRNFLTC SALFLALPAA AQVVYLHESD GYNGAINNKS LEPKITCYPE
 51 GTSYIFLDDV RISNVKHDQE DAGVFINRSG NLFFMGNRCN FTFHNLMTEG
101 FGAAISNRVG DTTLTLSNFS YLAFTSAPLL PQGQGAIYSL GSVMIENSEE
151 VTFCGNYSSW SGAAIYTPYL LGSKASRPSV NLSGNRYLVF RDNVSQVYGG
201 AISTHNLTLT TRGPSCFENN HAYHDVNSNG GAIAIAPGGS ISISVKSGDL
251 IFKGNTASQD GNTIHNSIHL QSGAQFKNLR AVSESGVYFY DPISHSESHK
301 ITDLVINAPE GKETYEGTIS FSGLCLDDHE VCAENLTSTI LQDVTLAGGT
351 LSLSDGVTLQ LHSFKQEASS TLTMSPGTTL LCSGDARVQN LHILIEDTDN
401 FVPVRIRAED KDALVSLEKL KVAFEAYWSV YDFPQFKEAF TIPLLELLGP
451 SFDSLLLGET TLERTQVTTE NDAVRGFWSL SWEEYPPSLD KDRRITPTKK
501 TVFLTWNPEI TSTP
```

Possible T cell epitope:

640 QLYVDWTPV

Possible B cell epitope:

482 WEEYPPSLDKDRRITPTKK

Figure 24: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 24; ORF: cpn100985

```
  1 MGISLPELFS NLGSAYLDYI FQHPPAYVWS VFLLLLARLL PIFAVAPFLG
 51 AKLFPSPIKI GISLSWLAII FPKVLADTQI TNYMDNNLFY VLLVKEMIIG
101 IVIGFVLAFP FYAAQSAGSF ITNQQGIQGL EGATSLISIE QTSPHGILYH
151 YFVTIIFWLV GGHRIVISLL LQTLEVIPIH SFFPAEMMSL SAPIWITMIK
201 MCQLCLVMTI QLSAPAALAM LMSDLFLGII NRMAPQVQVI YLLSALKAFM
251 GLLFLTLAWW FIIKQIDYFT LAWFKEVPIM LLGSNPQVL
```

Possible T cell epitope:

```
83   YMDNNLFYV
```

Possible B cell epitope:

```
78   TQITNYMDNN
```

Figure 25: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 25; ORF: cpn100987

```
  1 MKHSKEDDLS RFLPKNLLVE SPHPEEIPLK SLSFTMSWLP TIHPSWITIA
 51 MKEFPPEIQG QLLAWLPEPL VQEILPLLPG ISIAPHRCAP FGAFYLLDML
101 SKKIRPCGIT EEIFLPASSA NAILYYTGPV KIALINCLGL YSIAKELKHI
151 LDKVVIERVK NALSPTEKLF LTYCQSHPMK HLETTNFLSS WTTDAELRQF
201 VHKQGLEFLG KALTKENASF LWYFLRRLDV GRAYIVEQTL KTWYDHPYVD
251 YFKSRLEQCM KVLVK
```

Possible T cell epitope:

220 FLWYFLRRL

Possible B cell epitope:

1 MKHSKEDDLSR

Figure 26: Identification of T- and B-cell epitopes from the amino acid sequences SEQ ID No. 26; ORF: cpn100988

```
  1 MLAFFATSFK SVLFEYSYQS LLLILIVSAP PIILASIVGI MVAIFQAATQ
 51 IQEQTFAFAV KLVVIFGTLM ISGGWLSNMI LRFAGQIFQN FYKWK
```

Possible T cell epitope:

21 LLLILIVSA

Possible B cell epitope:

89 QNFYKWK

77813-73/ccm

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that: my residence, post office address and citizenship are as stated below next to my name; that I verily believe that I am the original, first and sole inventor (if only one name is listed below) or a joint inventor (if plural inventors are named below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES THEREOF

the specification of which

☐ is attached hereto.

☒ was filed on June 21, 2001

as U.S. Application Serial No. 09/868,987

☒ was filed on December 23, 1999

as PCT International Application No. PCT/CA99/01230

and (if applicable) was amended on February 13, 2001

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information known to me which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §§1.56(a) and (b), which state:

"(a) A patent by its very nature is affected with a public interest. The public interest is best served, and the most effective patent examination occurs when, at the time an application is being examined, the Office is aware of and evaluates the teachings of all information material to patentability. Each individual associated with the filing and prosecution of a patent application has a duty of candor and good faith in dealing with the Office, which includes a duty to disclose to the Office all information known to that individual to be material to patentability as defined in this section. The duty to disclose information exists with respect to each pending claim until the claim is cancelled or withdrawn from consideration, or the application becomes abandoned. Information material to the patentability that is cancelled or withdrawn from consideration need not be submitted if the information is not material to the patentability of any claim remaining under consideration in the application. There is no duty to submit information which is not material to the patentability of any existing claim. The duty to disclose all information known to be material to patentability is deemed to be satisfied if all information known to be material to patentability of any claim issued in a patent was cited by the Office or submitted to the Office in the manner prescribed by §§1.97(b)-(d) and 1.98. However, no patent will be granted on an application in connection with which fraud on the Office was practiced or attempted or the duty of disclosure was violated through bad faith or intentional misconduct. The Office encourages applicants to carefully examine:

(1) prior art cited in search reports of a foreign patent office in a counterpart application,

(2) the closest information over which individuals associated with the filing or prosecution of a patent application believe any pending claim patentably defines, to make sure that any material information contained therein is disclosed to the Office.

(b) Under this section, information is material to patentability when it is not cumulative to information already of record or being made of record in the application, and

(1) It establishes, by itself or in combination with other information, a prima facie case of unpatentability of a claim; or

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A prima facie case of unpatentability is established when the information compels a conclusion that a claim is unpatentable under the preponderance of evidence, burden-of-proof standard, giving each term in the claim its broadest reasonable construction consistent with the specification, and before any consideration is given to evidence which may be submitted in an attempt to establish a contrary conclusion of patentability."

I hereby claim foreign priority benefits under 35 United States Code, §119 and/or §365 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate filed by me or my assignee disclosing the subject matter claimed in this application and having a filing date (1) before that of the application on which priority is claimed, or (2) if no priority claimed, before the filing of this application:

PRIOR FOREIGN APPLICATION(S)

Number	Country	Filing Date *(Day/Month/Year)*	Date First Laid-open or Published	Date Patented or Granted	Priority Claimed?

I hereby claim the benefit under 35 United States Code, §119(e) of any United States provisional application(s) listed below:

Application Number	Filing Date
60/113,280	December 23, 1998
60/113,281	December 23, 1998
60/113,282	December 23, 1998
60/113,283	December 23, 1998
60/113,284	December 23, 1998
60/113,285	December 23, 1998
60/113,385	December 23, 1998
60/114,050	December 28, 1998
60/114,056	December 28, 1998
60/114,057	December 28, 1998
60/114,058	December 28, 1998
60/114,059	December 28, 1998
60/114,061	December 28, 1998

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose information which is material to patentability as defined in

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PRIOR U.S. OR PCT APPLICATION(S)

Application No.	Filing Date *(day/month/year)*	Status *(pending, abandoned, granted)*

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that wilful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such wilful false statements may jeopardize the validity of the application or any patent issued thereon.

I hereby appoint the following patent agents with full power of substitution, association and revocation to prosecute this application and/or international application and to transact all business in the Patent and Trademark Office connected therewith:

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SEQUENCE LISTING

<110> Aventis Pasteur Limited

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

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Met Val Ser Ser Pro
1 5

att tta aac gtc cca ttg aaa aat cat gcc agt gtc tca ggg aaa ttt 163
Ile Leu Asn Val Pro Leu Lys Asn His Ala Ser Val Ser Gly Lys Phe
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acc cac cgt gaa gtg agc aaa ctc gcc tca gat tta aaa tct gga gcg 211
Thr His Arg Glu Val Ser Lys Leu Ala Ser Asp Leu Lys Ser Gly Ala
25 30 35

atg tct ttt gtt ccc gag gtt ctc agt gaa gag acg atc tct tct gat 259
Met Ser Phe Val Pro Glu Val Leu Ser Glu Glu Thr Ile Ser Ser Asp
40 45 50

ctt ggg aaa aaa caa tgt aca caa ggc att atc tca gca tgc tgt ggc 307
Leu Gly Lys Lys Gln Cys Thr Gln Gly Ile Ile Ser Ala Cys Cys Gly
55 60 65

ttg gca atg ctt att gtt ttg atg agc gta tat tat aga ttt gga ggc 355
Leu Ala Met Leu Ile Val Leu Met Ser Val Tyr Tyr Arg Phe Gly Gly
70 75 80 85

gtc atc gct tcg gga gct gtt ctt ctg aat ctt ttg ctt atc tgg gca 403
Val Ile Ala Ser Gly Ala Val Leu Leu Asn Leu Leu Leu Ile Trp Ala
90 95 100

gct cta cag tat ttg gat gcg cca ctc acc ttg tca gga ctc gct ggg 451
Ala Leu Gln Tyr Leu Asp Ala Pro Leu Thr Leu Ser Gly Leu Ala Gly
105 110 115

att gtt ctt gct atg ggg atg gcc gta gat gca aat gtt ctt gta ttc 499
Ile Val Leu Ala Met Gly Met Ala Val Asp Ala Asn Val Leu Val Phe
120 125 130

gaa aga atc cga gag gaa ttt tta ttg tct caa agt ctt aaa aaa tct 547
Glu Arg Ile Arg Glu Glu Phe Leu Leu Ser Gln Ser Leu Lys Lys Ser
135 140 145

gta gaa aaa gga tat acc aag gct ttt gga gcc att ttt gat tct aac 595
Val Glu Lys Gly Tyr Thr Lys Ala Phe Gly Ala Ile Phe Asp Ser Asn
150 155 160 165

ttg act aca gta ttg gcc tca gca ctt ctt ttc ttc cta gat aca ggg 643
Leu Thr Thr Val Leu Ala Ser Ala Leu Leu Phe Phe Leu Asp Thr Gly
170 175 180

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cct att aaa ggg ttt gct ttg aca ttg att tta gga att ttc tct tca     691
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atg ttt acg gct ctt ttc atg act aaa ttt ttc ttc atg ctg tgg atg     739
Met Phe Thr Ala Leu Phe Met Thr Lys Phe Phe Phe Met Leu Trp Met
        200                 205                 210

aat aag acc caa cat aca cag ttg cat atg atg aat aag ttc gtg ggg     787
Asn Lys Thr Gln His Thr Gln Leu His Met Met Asn Lys Phe Val Gly
    215                 220                 225

ata aag cat gat ttc ttg aga gga tgc aaa aaa ctt tgg gct gtt tct     835
Ile Lys His Asp Phe Leu Arg Gly Cys Lys Lys Leu Trp Ala Val Ser
230                 235                 240                 245

gga agt gtt ttt ctt tta ggt tgc gtt gct ctc ggg ttt gga gcc tgg     883
Gly Ser Val Phe Leu Leu Gly Cys Val Ala Leu Gly Phe Gly Ala Trp
                250                 255                 260

aat tcc gtt ttg gga atg gat ttt aaa gga ggg tat gcc ttt acc ttt     931
Asn Ser Val Leu Gly Met Asp Phe Lys Gly Gly Tyr Ala Phe Thr Phe
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aat cca aaa gag cat ggc atc agc gat gtt gct caa atg cgt ggc aaa     979
Asn Pro Lys Glu His Gly Ile Ser Asp Val Ala Gln Met Arg Gly Lys
        280                 285                 290

gtt gtg cat aaa cta cag gaa gct ggt ctt tct tct aga gac ttc cgt    1027
Val Val His Lys Leu Gln Glu Ala Gly Leu Ser Ser Arg Asp Phe Arg
    295                 300                 305

att caa aca ttt gga tct tca gaa aag atc aaa atc tat ttt agt gat    1075
Ile Gln Thr Phe Gly Ser Ser Glu Lys Ile Lys Ile Tyr Phe Ser Asp
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aaa gct tta agc tat act aag cag ata cga gcc tct ctc cta aaa tta    1123
Lys Ala Leu Ser Tyr Thr Lys Gln Ile Arg Ala Ser Leu Leu Lys Leu
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acg atc atg agc tgg cgt tat tgt ggg att gtt gtc aga aac agg cct    1171
Thr Ile Met Ser Trp Arg Tyr Cys Gly Ile Val Val Arg Asn Arg Pro
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aga ttt ctc tac gga aac tct aaa cga aac gca aaa ttt tgg tca aag    1219
Arg Phe Leu Tyr Gly Asn Ser Lys Arg Asn Ala Lys Phe Trp Ser Lys
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gta agc agc aaa cta tcg aag aaa atg cgt tat cag gcg acc atc ggg    1267
Val Ser Ser Lys Leu Ser Lys Lys Met Arg Tyr Gln Ala Thr Ile Gly
    375                 380                 385

ctt tta gga gct ttg gca atc atc ttg ctc tat gtg agt ttg cgc ttt    1315
Leu Leu Gly Ala Leu Ala Ile Ile Leu Leu Tyr Val Ser Leu Arg Phe
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ttg gct acc tgt gca gtc ttg ttt ata gca cat ttc ttt ttg aag aaa   1411
Leu Ala Thr Cys Ala Val Leu Phe Ile Ala His Phe Phe Leu Lys Lys
            425                 430                 435

att caa ata gat ttg caa gcc att ggt gct tta atg act gta ttg ggg   1459
Ile Gln Ile Asp Leu Gln Ala Ile Gly Ala Leu Met Thr Val Leu Gly
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tat tca tta aac aat act ttg atc att ttt gat cgt att cgt gaa gat   1507
Tyr Ser Leu Asn Asn Thr Leu Ile Ile Phe Asp Arg Ile Arg Glu Asp
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cgc caa gcg aac ctg ttt acc cct atg cat gtt tta gtt aat gat gcc   1555
Arg Gln Ala Asn Leu Phe Thr Pro Met His Val Leu Val Asn Asp Ala
470                 475                 480                 485

ctt caa aag acg ttc agc cgc acg gta atg aca aca gct aca act cta   1603
Leu Gln Lys Thr Phe Ser Arg Thr Val Met Thr Thr Ala Thr Thr Leu
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tca gtt ttg tta atg ctt ttg ttt ata ggc ggc tcc tct gtc ttt aat   1651
Ser Val Leu Leu Met Leu Leu Phe Ile Gly Gly Ser Ser Val Phe Asn
            505                 510                 515

ttt gca ttt att atg acc ata ggg att ctt cta gga act tta tcg tct   1699
Phe Ala Phe Ile Met Thr Ile Gly Ile Leu Leu Gly Thr Leu Ser Ser
        520                 525                 530

ctt tat att gca cca cct ctg ttg ttg ttt atg gtc cgt aaa gaa aat   1747
Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met Val Arg Lys Glu Asn
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cgc tca aaa taagtaccgt taaacttaat ctaacgtgta gcaatataaa           1796
Arg Ser Lys
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cat ccc gta gga gga aca gga aca gga gca gct gct cct gag tct gtg   163
His Pro Val Gly Gly Thr Gly Thr Gly Ala Ala Ala Pro Glu Ser Val
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cta aac ata gta gag gaa ata gca gca tcg ggg agt gtc acc gct ggt   211
Leu Asn Ile Val Glu Glu Ile Ala Ala Ser Gly Ser Val Thr Ala Gly
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cta caa gca att acg tcc agt cca gga atg gtg aat cta ctc ata gga   259
Leu Gln Ala Ile Thr Ser Ser Pro Gly Met Val Asn Leu Leu Ile Gly
          40                  45                  50

tgg gca aag aca aaa ttt att caa cct ata cgt gaa tca aag ctc ttt   307
Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg Glu Ser Lys Leu Phe
      55                  60                  65

caa tcc aga gct tgc caa att acc ctg ctc gtt tta gga att ctt ttg   355
Gln Ser Arg Ala Cys Gln Ile Thr Leu Leu Val Leu Gly Ile Leu Leu
  70                  75                  80                  85

gtt gtt gct gga tta gca tgt atg ttt atc ttc cat agc cag tta ggg   403
Val Val Ala Gly Leu Ala Cys Met Phe Ile Phe His Ser Gln Leu Gly
                  90                  95                 100

gca aat gca ttt tgg ttg att att cct gct gcc ata gga ttg att aag   451
Ala Asn Ala Phe Trp Leu Ile Ile Pro Ala Ala Ile Gly Leu Ile Lys
             105                 110                 115

tta cta gtt aca tca tta tgt ttt gat gaa gct tgt aca tct gaa aaa   499
Leu Leu Val Thr Ser Leu Cys Phe Asp Glu Ala Cys Thr Ser Glu Lys
         120                 125                 130

ctc atg gtt ttc caa aaa tgg gca ggt gtt tta gaa gat cag ctc gat   547
Leu Met Val Phe Gln Lys Trp Ala Gly Val Leu Glu Asp Gln Leu Asp
     135                 140                 145

gat ggg atc ctt aat aac tca aat aag att ttt ggc cat gtg aaa aca   595
Asp Gly Ile Leu Asn Asn Ser Asn Lys Ile Phe Gly His Val Lys Thr
150                 155                 160                 165

gaa gga aat acc tct agg gct act acc cca gta ctt aat gat ggc cgc   643
Glu Gly Asn Thr Ser Arg Ala Thr Thr Pro Val Leu Asn Asp Gly Arg
                 170                 175                 180

gga act cct gta ctt tca cct tta gta agt aaa ata gct cgc gtt       688
Gly Thr Pro Val Leu Ser Pro Leu Val Ser Lys Ile Ala Arg Val
             185                 190                 195

tagacgttca tctcacaagc atcctagaac ttgggatgct actttccacg tacgagatca 748

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Met Thr Ile Arg Ile
1 5

ctt gct gaa ggc cta gct ttc cgt tac gga agc aag gga ccg aat atc 163
Leu Ala Glu Gly Leu Ala Phe Arg Tyr Gly Ser Lys Gly Pro Asn Ile
10 15 20

att cat gat gtt tct ttc tct gtc tat gat ggc gac ttt ata gga atc 211
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ata gga cca aac gga ggg ggg aaa agc acc tta acg atg tta att ttg 259
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40 45 50

ggc ttg ctt act cct aca ttc gga tcc ttg aag act ttc cct tcg cat 307
Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys Thr Phe Pro Ser His
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tcc gcg ggg aaa caa acc cat tcc atg atc ggt tgg gtt ccc caa cat 355
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70 75 80 85

ttc tct tat gat cct tgt ttt cct atc tca gta aaa gat gtt gtc ctc 403
Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val Lys Asp Val Val Leu
90 95 100

tca gga aga ttg tct caa ctc tcc tgg cat gga aaa tat aaa aag aaa 451
Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly Lys Tyr Lys Lys Lys
105 110 115

gat ttt gaa gct gta gat cac gct ttg gat ctt gtt gga ctt tct gac 499
Asp Phe Glu Ala Val Asp His Ala Leu Asp Leu Val Gly Leu Ser Asp
120 125 130

acc acc acc act gct ttc gcc cat ctc tca gga gga caa atc cag cgt 547
Thr Thr Thr Thr Ala Phe Ala His Leu Ser Gly Gly Gln Ile Gln Arg
135 140 145

gta ctt ctg gca aga gcc tta gcc tcc tac cct gaa att tta att ctt 595
Val Leu Leu Ala Arg Ala Leu Ala Ser Tyr Pro Glu Ile Leu Ile Leu
150 155 160 165

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gat gag ccg acg aca aac att gat cct gac aat caa caa aga att tta   643
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                170                 175                 180

agt atc cta aaa aag ctc aac cgt acg tgc acc att ctt atg gta act   691
Ser Ile Leu Lys Lys Leu Asn Arg Thr Cys Thr Ile Leu Met Val Thr
            185                 190                 195

cac gat ctt cac cat acg acg aat tac ttt aat aaa gtt ttt tat atg   739
His Asp Leu His His Thr Thr Asn Tyr Phe Asn Lys Val Phe Tyr Met
        200                 205                 210

aac aaa act ttg cac ttc att ggc aga cac ttc gac ctt aac aga cca   787
Asn Lys Thr Leu His Phe Ile Gly Arg His Phe Asp Leu Asn Arg Pro
    215                 220                 225

att ttg ttg tca tcc tat aaa aat cag gaa ttt tca tgc tct cct cac   835
Ile Leu Leu Ser Ser Tyr Lys Asn Gln Glu Phe Ser Cys Ser Pro His
230                 235                 240                 245

taatccgtga ttcatttccc cttcttattt tacttcccac attcctagcg gcattaggag 895
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                                            Met His Lys Val Ile
                                              1               5

gtt ttc att ttc ctt acc cta tat tcg tta aaa agt tat ggg aat gat   163
Val Phe Ile Phe Leu Thr Leu Tyr Ser Leu Lys Ser Tyr Gly Asn Asp
                10                  15                  20

gta ata gat aag ccc cat gtt ctt gtc agt atc gcc ccc tat aaa ttc   211
Val Ile Asp Lys Pro His Val Leu Val Ser Ile Ala Pro Tyr Lys Phe
            25                  30                  35

cta gtt gaa caa att gct gaa gag acc tgt ttt gtc tat gcg ata gtt   259
Leu Val Glu Gln Ile Ala Glu Glu Thr Cys Phe Val Tyr Ala Ile Val
        40                  45                  50

acg aat cac tat gat ccc cat acc tat gaa ctt cct cct cag caa atc   307
Thr Asn His Tyr Asp Pro His Thr Tyr Glu Leu Pro Pro Gln Gln Ile
    55                  60                  65
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aag gag tta cga caa gga gac ctt tgg ttc cgt ata gga gag gca ttt   355
Lys Glu Leu Arg Gln Gly Asp Leu Trp Phe Arg Ile Gly Glu Ala Phe
 70                  75                  80                  85

gga aaa aac ttg tta gag aaa cct tac atg caa caa gtc gat ctt tcc   403
Gly Lys Asn Leu Leu Glu Lys Pro Tyr Met Gln Gln Val Asp Leu Ser
                90                  95                 100

caa aat gtc tcg ctg att caa gga aag cct tgc tgt aat caa cat acc   451
Gln Asn Val Ser Leu Ile Gln Gly Lys Pro Cys Cys Asn Gln His Thr
            105                 110                 115

acg aac tac gac acc cac act tgg tta agc cct aaa aac ctt aaa gtc   499
Thr Asn Tyr Asp Thr His Thr Trp Leu Ser Pro Lys Asn Leu Lys Val
        120                 125                 130

caa gtg gag act atc gtt acc act tta agt aaa aaa tat cct caa cac   547
Gln Val Glu Thr Ile Val Thr Thr Leu Ser Lys Lys Tyr Pro Gln His
    135                 140                 145

gcg act cta tat caa agc aat gga gag aaa ctt ctg tta gct ttg gac   595
Ala Thr Leu Tyr Gln Ser Asn Gly Glu Lys Leu Leu Leu Ala Leu Asp
150                 155                 160                 165

caa ctc aat gag gaa att ctt acg att acc tcc aaa gcg aaa caa cgc   643
Gln Leu Asn Glu Glu Ile Leu Thr Ile Thr Ser Lys Ala Lys Gln Arg
                170                 175                 180

cat att tta gtt tcc cat gga gcc ttt ggg tat ttt tgc cgt gat tac   691
His Ile Leu Val Ser His Gly Ala Phe Gly Tyr Phe Cys Arg Asp Tyr
            185                 190                 195

aat ttc tct cag cac act ata gag aaa agc agt cat gtt gag cct tct   739
Asn Phe Ser Gln His Thr Ile Glu Lys Ser Ser His Val Glu Pro Ser
        200                 205                 210

cct aaa gat gtg gct cgc gta ttt cgt gac att gaa cag tac aaa att   787
Pro Lys Asp Val Ala Arg Val Phe Arg Asp Ile Glu Gln Tyr Lys Ile
    215                 220                 225

tct tct gtg att ctt ctc gaa tac tct gga aga cga agt agt gct atg   835
Ser Ser Val Ile Leu Leu Glu Tyr Ser Gly Arg Arg Ser Ser Ala Met
230                 235                 240                 245

ctg gca gat cgt ttc cac atg cat act gtg aat ctc gat ccc tat gcg   883
Leu Ala Asp Arg Phe His Met His Thr Val Asn Leu Asp Pro Tyr Ala
                250                 255                 260

gaa aat gta ctt gta aac tta aaa acc ata gcg acg act ttt tct agt   931
Glu Asn Val Leu Val Asn Leu Lys Thr Ile Ala Thr Thr Phe Ser Ser
            265                 270                 275

tta tgacaatacg aattcttgct gaaggcctag ctttccgtta cggaagcaag        984
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Gly Gly Ile Ala Ile Asn Asn Val Ile Ile Asp Phe Ser Glu Ile Val
15 20 25 30

cct act aaa gat aat gca aca gta gct cca ccc act ctt aaa tta gta 147
Pro Thr Lys Asp Asn Ala Thr Val Ala Pro Pro Thr Leu Lys Leu Val
35 40 45

tcg aga act aat gca gat agt aaa gat aag att gat att aca gga act 195
Ser Arg Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp Ile Thr Gly Thr
50 55 60

gtg act ctt cta gat cct aat ggc aac tta tat caa aat tct tat ctt 243
Val Thr Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln Asn Ser Tyr Leu
65 70 75

ggt gaa gac cgc gat atc act ctt ttc aat ata gac aat tct gca agt 291
Gly Glu Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp Asn Ser Ala Ser
80 85 90

ggg gca gtt aca gcc acg aat gtc acc ctt caa ggg aat tta gga gct 339
Gly Ala Val Thr Ala Thr Asn Val Thr Leu Gln Gly Asn Leu Gly Ala
95 100 105 110

aaa aaa gga tat tta gga acc tgg aat ttg gat cca aat tcc tcg ggt 387
Lys Lys Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro Asn Ser Ser Gly
115 120 125

tca aaa att att cta aaa tgg acc ttt gac aaa tac ctg cgc tgg ccc 435
Ser Lys Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr Leu Arg Trp Pro
130 135 140

tac atc cct aga gac aac cac ttc tac atc aac tct att tgg gga gca 483
Tyr Ile Pro Arg Asp Asn His Phe Tyr Ile Asn Ser Ile Trp Gly Ala
145 150 155

caa aac tct tta gtg act gtg aac caa ggg atc tta ggg aac atg ttg 531
Gln Asn Ser Leu Val Thr Val Asn Gln Gly Ile Leu Gly Asn Met Leu
160 165 170

aac aat gca agg ttt gaa gat cct gct ttc aac aac ttc tgg gct tcg 579
Asn Asn Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn Phe Trp Ala Ser
175 180 185 190

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gct ata gga tct ttc ctt agg aaa gaa gta tct cga aat tct gac tca   627
Ala Ile Gly Ser Phe Leu Arg Lys Glu Val Ser Arg Asn Ser Asp Ser
                195                 200                 205

ttc acc tat cat ggc aga ggc tat acc gct gct gtg gat gcc aaa cct   675
Phe Thr Tyr His Gly Arg Gly Tyr Thr Ala Ala Val Asp Ala Lys Pro
            210                 215                 220

cgc caa gaa ttt att tta gga gct gcc ttc agt cag gtt ttt ggt cac   723
Arg Gln Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln Val Phe Gly His
        225                 230                 235

gcc gag tct gaa tat cac ctt gac aac tat aag cat aaa ggc tca ggt   771
Ala Glu Ser Glu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly
    240                 245                 250

cac tct aca caa gca tct ctt tat gct ggc aat atc ttc tat ttt cct   819
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255                 260                 265                 270

gcg ata cgg tct cgg cct att cta ttc caa ggt gtg gcg acc tat ggt   867
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Tyr Met Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser Ile Glu Glu Lys
            290                 295                 300

aat atg gca aac tgg gat agc att gct tgg tta ttt gat ctg cgt ttc   963
Asn Met Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe Asp Leu Arg Phe
        305                 310                 315

agt gtg gat ctt aaa gaa cct caa cct cac tct aca gca agg ctt acc   1011
Ser Val Asp Leu Lys Glu Pro Gln Pro His Ser Thr Ala Arg Leu Thr
    320                 325                 330

ttc tat aca gaa gct gag tat acc aga att cgc cag gag aaa ttc aca   1059
Phe Tyr Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln Glu Lys Phe Thr
335                 340                 345                 350

gag cta gac tat gat cct aga tct ttc tct gca tgc tct tat gga aac   1107
Glu Leu Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys Ser Tyr Gly Asn
                355                 360                 365

tta gca att cct act gga ttc tct gta gac gga gca tta gct tgg cgt   1155
Leu Ala Ile Pro Thr Gly Phe Ser Val Asp Gly Ala Leu Ala Trp Arg
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gag att att cta tat aat aaa gta tca gct gcg tac ctc cct gtg att   1203
Glu Ile Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr Leu Pro Val Ile
        385                 390                 395

ctc agg aat aat cca aaa gcg acc tat gaa gtt ctc tct aca aaa gaa   1251
Leu Arg Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu Ser Thr Lys Glu
    400                 405                 410
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415 420 425 430

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Glu Val Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp Thr Leu Tyr Gly
435 440 445

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Thr Tyr Thr Ile Asp Ala Ser Met Asn Thr Leu Val Gln Met Ala Asn
450 455 460

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Gly Gly Ile Arg Phe Val Phe
465

tgaggatacg gagagagtgg gattcgaacc cacggtacgc gttaacgcac acacgctttc 1506
caagcgtgct ccttaagcca ctcggacatc tctccatatt tata 1550

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<212> DNA
<213> Chlamydia pneumoniae

<220>
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<222> (101)..(2866)

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Met Arg Phe Ser Leu
1 5

tgc gga ttt cct cta gtt ttt tct ttt aca ttg ctc tca gtc ttc gac 163
Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu Leu Ser Val Phe Asp
10 15 20

act tct ttg agt gct act acg att tct tta acc cca gaa gat agt ttt 211
Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr Pro Glu Asp Ser Phe
25 30 35

cat gga gat agt cag aat gca gaa cgt tct tat aat gtt caa gct ggg 259
His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr Asn Val Gln Ala Gly
40 45 50

gat gtc tat agc ctt act ggt gat gtc tca ata tct aac gtc gat aac 307
Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile Ser Asn Val Asp Asn
55 60 65

tct gca tta aat aaa gcc tgc ttc aat gtg acc tca gga agt gtg acg 355
Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr Ser Gly Ser Val Thr
70 75 80 85

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ttc gca gga aat cat cat ggg tta tat ttt aat aat att tcc tca gga   403
Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn Asn Ile Ser Ser Gly
                 90                  95                 100

act aca aag gaa ggg gct gta ctt tgt tgc caa gat cct caa gca acg   451
Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln Asp Pro Gln Ala Thr
            105                 110                 115

gca cgt ttt tct ggg ttc tcc acg ctc tct ttt att cag agc ccc gga   499
Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe Ile Gln Ser Pro Gly
        120                 125                 130

gat att aaa gaa cag gga tgt ctc tat tca aaa aat gca ctt atg ctc   547
Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys Asn Ala Leu Met Leu
    135                 140                 145

tta aac aat tat gta gtg cgt ttt gaa caa aac caa agt aag act aaa   595
Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn Gln Ser Lys Thr Lys
150                 155                 160                 165

ggc gga gct att agt ggg gcg aat gtt act ata gta ggc aac tac gat   643
Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile Val Gly Asn Tyr Asp
                170                 175                 180

tcc gtc tct ttc tat cag aat gca gcc act ttt gga ggt gct atc cat   691
Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe Gly Gly Ala Ile His
            185                 190                 195

tct tca ggt ccc cta cag att gca gta aat cag gca gag ata aga ttt   739
Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln Ala Glu Ile Arg Phe
        200                 205                 210

gca caa aat act gcc aag aat ggt tct gga ggg gct ttg tac tcc gat   787
Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly Ala Leu Tyr Ser Asp
    215                 220                 225

ggt gat att gat att gat cag aat gct tat gtt cta ttt cga gaa aat   835
Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val Leu Phe Arg Glu Asn
230                 235                 240                 245

gag gca ttg act act gct ata ggt aag gga ggg gct gtc tgt tgt ctt   883
Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly Ala Val Cys Cys Leu
                250                 255                 260

ccc act tca gga agt agt act cca gtt cct att gtg act ttc tct gac   931
Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile Val Thr Phe Ser Asp
            265                 270                 275

aat aaa cag tta gtc ttt gaa aga aac cat tcc ata atg ggt ggc gga   979
Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser Ile Met Gly Gly Gly
        280                 285                 290

gcc att tat gct agg aaa ctt agc atc tct tca gga ggt cct act cta  1027
Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser Gly Gly Pro Thr Leu
    295                 300                 305
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ttt atc aat aat ata tca tat gca aat tcg caa aat tta ggt gga gct   1075
Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln Asn Leu Gly Gly Ala
310                 315                 320                 325

att gcc att gat act gga ggg gag atc agt tta tca gca gag aaa gga   1123
Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu Ser Ala Glu Lys Gly
                330                 335                 340

aca att aca ttc caa gga aac cgg acg agc tta ccg ttt ttg aat ggc   1171
Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu Pro Phe Leu Asn Gly
            345                 350                 355

atc cat ctt tta caa aat gct aaa ttc ctg aaa tta cag gcg aga aat   1219
Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys Leu Gln Ala Arg Asn
        360                 365                 370

gga tac tct ata gaa ttt tat gat cct att act tct gaa gca gat ggg   1267
Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr Ser Glu Ala Asp Gly
    375                 380                 385

tct acc caa ttg aat atc aac gga gat cct aaa aat aaa gag tac aca   1315
Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys Asn Lys Glu Tyr Thr
390                 395                 400                 405

ggg acc ata ctc ttt tct gga gaa aag agt cta gca aac gat cct agg   1363
Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu Ala Asn Asp Pro Arg
                410                 415                 420

gat ttt aaa tct aca atc cct cag aac gtc aac ctg tct gca gga tac   1411
Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn Leu Ser Ala Gly Tyr
            425                 430                 435

tta gtt att aaa gag ggg gcc gaa gtc aca gtt tca aaa ttc acg cag   1459
Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val Ser Lys Phe Thr Gln
        440                 445                 450

tct cca gga tcg cat tta gtt tta gat tta gga acc aaa ctg ata gcc   1507
Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly Thr Lys Leu Ile Ala
    455                 460                 465

tct aag gaa gac att gcc atc aca ggc ctc gcg ata gat ata gat agc   1555
Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala Ile Asp Ile Asp Ser
470                 475                 480                 485

tta agc tca tcc tca aca gca gct gtt att aaa gca aac acc gca aat   1603
Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys Ala Asn Thr Ala Asn
                490                 495                 500

aaa cag ata tcc gtg acg gac tct ata gaa ctt atc tcg cct act ggc   1651
Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu Ile Ser Pro Thr Gly
            505                 510                 515

aat gcc tat gaa gat ctc aga atg aga aat tca cag acg ttc cct ctg   1699
Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser Gln Thr Phe Pro Leu
        520                 525                 530
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ctc tct tta gag cct gga gcc ggg ggt agt gtg act gta act gct gga     1747
Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val Thr Val Thr Ala Gly
    535                 540                 545

gat ttc cta ccg gta agt ccc cat tat ggt ttt caa ggc aat tgg aaa     1795
Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe Gln Gly Asn Trp Lys
550                 555                 560                 565

tta gct tgg aca gga act gga aac aaa gtt gga gaa ttc ttc tgg gat     1843
Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly Glu Phe Phe Trp Asp
                570                 575                 580

aaa ata aat tat aag cct aga cct gaa aaa gaa gga aat tta gtt cct     1891
Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu Gly Asn Leu Val Pro
            585                 590                 595

aat atc ttg tgg ggg aat gct gta gat gtc aga tcc tta atg cag gtt     1939
Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg Ser Leu Met Gln Val
        600                 605                 610

caa gag acc cat gca tcg agc tta cag aca gat cga ggg ctg tgg atc     1987
Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp Arg Gly Leu Trp Ile
    615                 620                 625

gat gga att ggg aat ttc ttc cat gta tct gcc tcc gaa gac aat ata     2035
Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala Ser Glu Asp Asn Ile
630                 635                 640                 645

agg tac cgt cat aac agc ggt gga tat gtt cta tct gta aat aat gag     2083
Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu Ser Val Asn Asn Glu
                650                 655                 660

atc aca cct aag cac tat act tcg atg gca ttt tcc caa ctc ttt agt     2131
Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe Ser Gln Leu Phe Ser
            665                 670                 675

aga gac aag gac tat gcg gtt tcc aac aac gaa tac aga atg tat tta     2179
Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu Tyr Arg Met Tyr Leu
        680                 685                 690

gga tcg tat ctc tat caa tat aca acc tcc cta ggg aat att ttc cgt     2227
Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu Gly Asn Ile Phe Arg
    695                 700                 705

tat gct tcg cgt aac cct aat gta aac gtc ggg att ctc tca aga agg     2275
Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly Ile Leu Ser Arg Arg
710                 715                 720                 725

ttt ctt caa aat cct ctt atg att ttt cat ttt ttg tgt gct tat ggt     2323
Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe Leu Cys Ala Tyr Gly
                730                 735                 740

cat gcc acc aat gat atg aaa aca gac tac gca aat ttc cct atg gtg     2371
His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala Asn Phe Pro Met Val
            745                 750                 755
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aaa aac agc tgg aga aac aat tgt tgg gct ata gag tgc gga ggg agc   2419
Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile Glu Cys Gly Gly Ser
        760                 765                 770

atg cct cta ttg gta ttt gag aac gga aga ctt ttc caa ggt gcc atc   2467
Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu Phe Gln Gly Ala Ile
    775                 780                 785

cca ttt atg aaa cta caa tta gtt tat gct tat cat gga gat ttc aaa   2515
Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr His Gly Asp Phe Lys
790                 795                 800                 805

gag acg act gca gat ggc cgt aga ttt agt aat ggg agt tta aca tcg   2563
Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn Gly Ser Leu Thr Ser
                810                 815                 820

att tct gta cct cta ggc ata cgc ttt gag aag ctg gca ctt tct cag   2611
Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys Leu Ala Leu Ser Gln
            825                 830                 835

gat gta ctc tat gac ttt agt ttc tcc tat att cct gat att ttc cgt   2659
Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile Pro Asp Ile Phe Arg
        840                 845                 850

aag gat ccc tca tgt gaa gct gct ctg gtg att agc gga gac tcc tgg   2707
Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile Ser Gly Asp Ser Trp
    855                 860                 865

ctt gtt ccg gca gca cac gta tca aga cat gct ttt gta ggg agt gga   2755
Leu Val Pro Ala Ala His Val Ser Arg His Ala Phe Val Gly Ser Gly
870                 875                 880                 885

acg ggt cgg tat cac ttt aac gac tat act gag ctc tta tgt cga gga   2803
Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu Leu Leu Cys Arg Gly
                890                 895                 900

agt ata gaa tgc cgc ccc cat gct agg aat tat aat ata aac tgt gga   2851
Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr Asn Ile Asn Cys Gly
            905                 910                 915

agc aaa ttt cgt ttt tagaaggttt ccattgcctg tgtggttccg gatcttaact   2906
Ser Lys Phe Arg Phe
        920

ataaatcctg gactatggat cataggcatt gggtttctcg aact                 2950
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<210> 7
<211> 1328
<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (101)..(1225)

<220>
<221> unsure

<222> (1254)...(1323)
<223> n is a or g or c or t/u, unknown, or other

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agcaaccaag caaagaaagg tggtggggtt tatcttgaag atg ccc tca tcc tgg 115
Met Pro Ser Ser Trp
1 5

aaa agg tta tta cag gtt ctg tct cac aaa ata gca gct aca gaa agt 163
Lys Arg Leu Leu Gln Val Leu Ser His Lys Ile Ala Ala Thr Glu Ser
10 15 20

ggt ggg ggt atc tac gct aag gat att caa cta caa gct cta cct gga 211
Gly Gly Gly Ile Tyr Ala Lys Asp Ile Gln Leu Gln Ala Leu Pro Gly
25 30 35

agc ttc aca att acc gat aat aaa gtc gaa act agt ctt act act agc 259
Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr Ser Leu Thr Thr Ser
40 45 50

act aat tta tat ggt ggg ggc atc tat tcc agt gga gct gtc acg cta 307
Thr Asn Leu Tyr Gly Gly Gly Ile Tyr Ser Ser Gly Ala Val Thr Leu
55 60 65

acc aat ata tct gga acc ttt ggc att aca gga aac tct gtt atc aat 355
Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly Asn Ser Val Ile Asn
70 75 80 85

aca gcg aca tcc cag gat gca gat ata caa ggt ggg ggc att tat gca 403
Thr Ala Thr Ser Gln Asp Ala Asp Ile Gln Gly Gly Gly Ile Tyr Ala
90 95 100

acc acg tct ctc tca ata aat caa tgt aat aca ccc att cta ttt agc 451
Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr Pro Ile Leu Phe Ser
105 110 115

aac aac tct gct gcc act aaa aaa aca tca aca aca aag caa att gct 499
Asn Asn Ser Ala Ala Thr Lys Lys Thr Ser Thr Thr Lys Gln Ile Ala
120 125 130

ggt ggg gct atc ttc tcc gct gca gta act atc gag aat aac tct cag 547
Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile Glu Asn Asn Ser Gln
135 140 145

ccc att att ttc tta aat aat tcc gca aag tcg gaa gca act aca gca 595
Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser Glu Ala Thr Thr Ala
150 155 160 165

gca act gca gga aat aaa gat agc tgt gga gga gcc att gca gct aac 643
Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly Ala Ile Ala Ala Asn
170 175 180

tct gtt act tta aca aat aac cct gaa ata acc ttt aaa gga aat tat 691
Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr Phe Lys Gly Asn Tyr
185 190 195

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gca gaa act gga gga gcg att ggc tgt att gat ctt act aat ggc tca   739
Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp Leu Thr Asn Gly Ser
        200                 205                 210

cct ccc cgt aaa gtc tct att gca gac aac ggt tct gtc ctt ttt caa   787
Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly Ser Val Leu Phe Gln
    215                 220                 225

gac aac tct gcg tta aat cgc gga ggc gct atc tat gga gag act atc   835
Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile Tyr Gly Glu Thr Ile
230                 235                 240                 245

gat atc tcc agg aca ggt gcg act ttc atc ggt aac tct tca aaa cat   883
Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly Asn Ser Ser Lys His
                250                 255                 260

gat gga agt gca att tgc tgt tca aca gcc cta act ctt gcg cca aac   931
Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu Thr Leu Ala Pro Asn
            265                 270                 275

tcc caa ctt atc ttt gaa aac aat aag gtt acg gaa acc aca gcc act   979
Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr Glu Thr Thr Ala Thr
        280                 285                 290

aca aaa gct tcc ata aat aat tta gga gct gca att tat gga aat aat  1027
Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala Ile Tyr Gly Asn Asn
    295                 300                 305

gag act agt gac gtc act atc tct tta tca gct gag aat gga agt att  1075
Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala Glu Asn Gly Ser Ile
310                 315                 320                 325

ttc ttt aaa aac aat cta tgc aca gca aca aac aaa tac tgc agt att  1123
Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn Lys Tyr Cys Ser Ile
                330                 335                 340

gct gga aac gta aaa ttt aca gca ata gaa gct tca gca ggg aaa gct  1171
Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala Ser Ala Gly Lys Ala
            345                 350                 355

ata tct ttc tat gat gca gtt aac gtt cca cca aag aaa caa ttg ctc  1219
Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro Lys Lys Gln Leu Leu
        360                 365                 370

aag agc taaattaaat gaaaaagcga caagtacang gacgtttcta ntttctgggg  1275
Lys Ser
    375

gacttcacgg aaataaatcc ctattccaca gaaagtcact tcgccctngg gat      1328
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<210> 8
<211> 2816
<212> DNA
<213> Chlamydia pneumoniae

<220>
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atgggagtat ttttgataaa aagcttttcc ccaaagacac atg aaa tat tct tta 115
Met Lys Tyr Ser Leu
1 5

cct tgg cta ctt acc tct tcg gct tta gtt ttc tcc cta cat cca cta 163
Pro Trp Leu Leu Thr Ser Ser Ala Leu Val Phe Ser Leu His Pro Leu
10 15 20

atg gct gct aac acg gat ctc tca tca tcc gat aac tat gaa aat ggt 211
Met Ala Ala Asn Thr Asp Leu Ser Ser Ser Asp Asn Tyr Glu Asn Gly
25 30 35

agt agt ggt agc gca gca ttc act gcc aag gaa act tcg gat gct tca 259
Ser Ser Gly Ser Ala Ala Phe Thr Ala Lys Glu Thr Ser Asp Ala Ser
40 45 50

gga act acc tac act ctc act agc gat gtt tct att acg aat gta tct 307
Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser Ile Thr Asn Val Ser
55 60 65

gca att act cct gca gat aaa agc tgt ttt aca aac aca gga gga gca 355
Ala Ile Thr Pro Ala Asp Lys Ser Cys Phe Thr Asn Thr Gly Gly Ala
70 75 80 85

ttg agt ttt gtt gga gct gat cac tca ttg gtt ctg caa acc ata gcg 403
Leu Ser Phe Val Gly Ala Asp His Ser Leu Val Leu Gln Thr Ile Ala
90 95 100

ctt acg cat gat ggt gct gca att aac aat acc aac aca gct ctt tct 451
Leu Thr His Asp Gly Ala Ala Ile Asn Asn Thr Asn Thr Ala Leu Ser
105 110 115

ttc tca gga ttc tcg tca ctc tta atc gac tca gct cca gca aca gga 499
Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser Ala Pro Ala Thr Gly
120 125 130

act tcg ggc ggc aag ggt gct att tgt gtg aca aat aca gag gga ggt 547
Thr Ser Gly Gly Lys Gly Ala Ile Cys Val Thr Asn Thr Glu Gly Gly
135 140 145

act gcg act ttt act gac aat gcc agt gtc acc ctc caa aaa aat act 595
Thr Ala Thr Phe Thr Asp Asn Ala Ser Val Thr Leu Gln Lys Asn Thr
150 155 160 165

tca gaa aaa gat gga gct gca gtt tct gcc tac agc atc gat ctt gct 643
Ser Glu Lys Asp Gly Ala Ala Val Ser Ala Tyr Ser Ile Asp Leu Ala
170 175 180

aag act acg aca gca gct ctc tta gat caa aat act agc aca aaa aat 691
Lys Thr Thr Thr Ala Ala Leu Leu Asp Gln Asn Thr Ser Thr Lys Asn
185 190 195

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ggc ggg gcc ctc tgt agt aca gca aac act aca gtc caa gga aac tca   739
Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr Val Gln Gly Asn Ser
        200                 205                 210

gga acg gtg acc ttc tcc tca aat act gct aca gat aaa ggt ggg ggg   787
Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr Asp Lys Gly Gly Gly
    215                 220                 225

atc tac tca aaa gaa aag gat agc acg cta gat gcc aat aca gga gtc   835
Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp Ala Asn Thr Gly Val
230                 235                 240                 245

gtt acc ttc aaa tct aat act gca aag acg ggg ggt gct tgg agc tct   883
Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly Gly Ala Trp Ser Ser
            250                 255                 260

gat gac aat ctt gct ctt acc ggc aac act caa gta ctt ttt cag gaa   931
Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln Val Leu Phe Gln Glu
        265                 270                 275

aat aaa aca acc ggc tca gca gca cag gca aat aac ccg gaa ggt tgt   979
Asn Lys Thr Thr Gly Ser Ala Ala Gln Ala Asn Asn Pro Glu Gly Cys
    280                 285                 290

ggt ggg gca atc tgt tgt tat ctt gct aca gca aca gac aaa act gga  1027
Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala Thr Asp Lys Thr Gly
295                 300                 305

tta gcc att tct cag aat caa gaa atg agc ttc act agt aat aca aca  1075
Leu Ala Ile Ser Gln Asn Gln Glu Met Ser Phe Thr Ser Asn Thr Thr
310                 315                 320                 325

act gcg aat ggt gga gcg atc tac gct act aaa tgt act ctg gat gga  1123
Thr Ala Asn Gly Gly Ala Ile Tyr Ala Thr Lys Cys Thr Leu Asp Gly
            330                 335                 340

aac aca act ctt acc ttc gat cag aat act gcg aca gca gga tgt ggc  1171
Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala Thr Ala Gly Cys Gly
        345                 350                 355

gga gct atc tat aca gaa act gaa gat ttt tct ctt aag gga agt acg  1219
Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser Leu Lys Gly Ser Thr
    360                 365                 370

gga acc gtg acc ttc agc aca aat aca gca aag aca ggc ggc gcc tta  1267
Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys Thr Gly Gly Ala Leu
375                 380                 385

tat tct aaa gga aac agc tcg ctg act gga aat acc aac ctg ctc ttt  1315
Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn Thr Asn Leu Leu Phe
390                 395                 400                 405

tca ggg aac aaa gct acg ggc ccg agt aat tct tca gca aat caa gag  1363
Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser Ser Ala Asn Gln Glu
            410                 415                 420
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ggt tgc ggt ggg gca atc cta gcc ttt att gat tca gga tcc gta agc 1411
Gly Cys Gly Gly Ala Ile Leu Ala Phe Ile Asp Ser Gly Ser Val Ser
425 430 435

gat aaa aca gga cta tcg att gca aac aac caa gaa gtc agc ctc act 1459
Asp Lys Thr Gly Leu Ser Ile Ala Asn Asn Gln Glu Val Ser Leu Thr
440 445 450

agt aat gct gca aca gta agt ggt ggt gcg atc tat gct acc aaa tgt 1507
Ser Asn Ala Ala Thr Val Ser Gly Gly Ala Ile Tyr Ala Thr Lys Cys
455 460 465

act cta act gga aac ggc tcc ctg acc ttt gac ggc aat act gct gga 1555
Thr Leu Thr Gly Asn Gly Ser Leu Thr Phe Asp Gly Asn Thr Ala Gly
470 475 480 485

act tca gga ggg gcg atc tat aca gaa act gaa gat ttt act ctt aca 1603
Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Thr Leu Thr
490 495 500

gga agt aca gga acc gtg acc ttc agc aca aat aca gca aag aca ggc 1651
Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys Thr Gly
505 510 515

ggc gcc tta tat tct aaa ggc aac aac tct ctg tct ggt aat acc aac 1699
Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu Ser Gly Asn Thr Asn
520 525 530

ctg ctc ttt tca ggg aac aaa gct acg ggc ccg agt aat tct tca gca 1747
Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser Ser Ala
535 540 545

aat caa gag ggt tgc ggt ggg gca atc cta tcg ttt ctt gag tca gca 1795
Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser Phe Leu Glu Ser Ala
550 555 560 565

tct gta agt act aaa aaa gga ctc tgg att gaa gat aac gaa aac gtg 1843
Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu Asp Asn Glu Asn Val
570 575 580

agt ctc tct ggt aat act gca aca gta agt ggc ggt gcg atc tat gcg 1891
Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly Gly Ala Ile Tyr Ala
585 590 595

acc aag tgt gct ctg cat gga aac acg act ctt acc ttt gat ggc aat 1939
Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu Thr Phe Asp Gly Asn
600 605 610

act gcc gaa act gca gga gga gcg atc tat aca gaa acc gaa gat ttt 1987
Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe
615 620 625

act ctt acg gga agt acg gga acc gtg acc ttc agc aca aat aca gca 2035
Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala
630 635 640 645

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aag aca gca ggg gct cta cat act aaa gga aat act tcc ttt acc aaa   2083
Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn Thr Ser Phe Thr Lys
                650                 655                 660

aat aag gct ctt gta ttt tct gga aat tca gca aca gca aca gca aca   2131
Asn Lys Ala Leu Val Phe Ser Gly Asn Ser Ala Thr Ala Thr Ala Thr
            665                 670                 675

aca act aca gat caa gaa ggt tgt ggt gga gcg atc ctc tgt aat atc   2179
Thr Thr Thr Asp Gln Glu Gly Cys Gly Gly Ala Ile Leu Cys Asn Ile
        680                 685                 690

tca gag tct gac ata gct aca aaa agc tta act ctt act gaa aat gag   2227
Ser Glu Ser Asp Ile Ala Thr Lys Ser Leu Thr Leu Thr Glu Asn Glu
    695                 700                 705

agt tta agt ttc att aac aat acg gca aaa aga agt ggt ggt ggt att   2275
Ser Leu Ser Phe Ile Asn Asn Thr Ala Lys Arg Ser Gly Gly Gly Ile
710                 715                 720                 725

tat gct cct aag tgt gta atc tca ggc agt gaa tcc ata aac ttt gat   2323
Tyr Ala Pro Lys Cys Val Ile Ser Gly Ser Glu Ser Ile Asn Phe Asp
                730                 735                 740

ggc aat act gct gaa act tcg gga gga gcg att tat tcg aaa aac ctt   2371
Gly Asn Thr Ala Glu Thr Ser Gly Gly Ala Ile Tyr Ser Lys Asn Leu
            745                 750                 755

tcg att aca gct aac ggt cct gtc tcc ttt acc aat aat tct gga ggc   2419
Ser Ile Thr Ala Asn Gly Pro Val Ser Phe Thr Asn Asn Ser Gly Gly
        760                 765                 770

aag gga ggc gcc att tat ata gcc gat agc gga gaa ctt tcc tta gag   2467
Lys Gly Gly Ala Ile Tyr Ile Ala Asp Ser Gly Glu Leu Ser Leu Glu
    775                 780                 785

gct att gat ggg gat att act ttc tca ggg aac cga gcg act gag gga   2515
Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn Arg Ala Thr Glu Gly
790                 795                 800                 805

act tca act ccc aac tcg atc cat tta ggt gcc agg ggc aag atc act   2563
Thr Ser Thr Pro Asn Ser Ile His Leu Gly Ala Arg Gly Lys Ile Thr
                810                 815                 820

aag ctt gca gca gct cct ggt cat acg att tat ttt tat gat cct att   2611
Lys Leu Ala Ala Ala Pro Gly His Thr Ile Tyr Phe Tyr Asp Pro Ile
            825                 830                 835

acg atg gaa gct cct gca tct gga gga aca ata gag gag tta gtc atc   2659
Thr Met Glu Ala Pro Ala Ser Gly Gly Thr Ile Glu Glu Leu Val Ile
        840                 845                 850

aat cct gtt gtc aaa gct att gtt cct cct ccc caa cca aaa aat ggt   2707
Asn Pro Val Val Lys Ala Ile Val Pro Pro Pro Gln Pro Lys Asn Gly
    855                 860                 865
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cct ata tagaagaaaa acgaatgctc tttgtaaggc tcaagagtaa aaaattctaa    2763
Pro Ile
870

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<222> (101)..(2989)

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taaatttata aacttctaga caacaaattg atgatttttt atg aca aac tct att   115
                                            Met Thr Asn Ser Ile
                                              1               5

ttc ata tca aag ttt gga tgt tta tgc gac cca ttt gtc tca gca ttt   163
Phe Ile Ser Lys Phe Gly Cys Leu Cys Asp Pro Phe Val Ser Ala Phe
                 10                  15                  20

tat ccc act gcg cta tgt tgt tcc tta tca gga aat gaa gtc cct aac   211
Tyr Pro Thr Ala Leu Cys Cys Ser Leu Ser Gly Asn Glu Val Pro Asn
             25                  30                  35

ctc gcc tct tgt cag atg tct aga aaa gac atc tct gct ttc cac acg   259
Leu Ala Ser Cys Gln Met Ser Arg Lys Asp Ile Ser Ala Phe His Thr
         40                  45                  50

tct cca agc ttc cgt ctg aat gta act cca gag ccc ttg gtt tcc tcc   307
Ser Pro Ser Phe Arg Leu Asn Val Thr Pro Glu Pro Leu Val Ser Ser
     55                  60                  65

ttt cgt ccc tct aat ctt ctt aat gga ttc ggt cac gat ata acc cag   355
Phe Arg Pro Ser Asn Leu Leu Asn Gly Phe Gly His Asp Ile Thr Gln
 70                  75                  80                  85

gac atc aca att aca gga aac tct atc aat tct gtt ata gat tat aac   403
Asp Ile Thr Ile Thr Gly Asn Ser Ile Asn Ser Val Ile Asp Tyr Asn
                 90                  95                 100

tac cac tac gag gat gga ggc att ctt gca tgt aaa aat ttg ttc att   451
Tyr His Tyr Glu Asp Gly Gly Ile Leu Ala Cys Lys Asn Leu Phe Ile
            105                 110                 115

tct gaa aat aaa gga aac tta agt ttt gaa agg aat agc tcc cac agt   499
Ser Glu Asn Lys Gly Asn Leu Ser Phe Glu Arg Asn Ser Ser His Ser
        120                 125                 130

tct gga ggg gct ctc tac agt gtt cgg gaa tgc tgg att tct aag aat   547
Ser Gly Gly Ala Leu Tyr Ser Val Arg Glu Cys Trp Ile Ser Lys Asn
    135                 140                 145
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cag aac tac tcg ttt att tca aat gcg gct tcc tta gct act act aca 595
Gln Asn Tyr Ser Phe Ile Ser Asn Ala Ala Ser Leu Ala Thr Thr Thr
150 155 160 165

act tca gga ttt ggt ggg gct ata cat gca cta gat agc tat att aca 643
Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu Asp Ser Tyr Ile Thr
170 175 180

aat aac tta gga gaa gga caa ttc tta gat aat gtc tct aaa aat aga 691
Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn Val Ser Lys Asn Arg
185 190 195

gga gga gct atc tat gtt ggg gtg agt tta tca atc aca gac aac tta 739
Gly Gly Ala Ile Tyr Val Gly Val Ser Leu Ser Ile Thr Asp Asn Leu
200 205 210

ggt cct atc gtt atc aag aaa aat caa aca tta gaa gat tcc agc ttt 787
Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu Glu Asp Ser Ser Phe
215 220 225

gga gga ggc atc ttc tgc aga gcc gta aat ata gaa agg aat tat caa 835
Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile Glu Arg Asn Tyr Gln
230 235 240 245

aac atc caa atc aat gat aat gct tca gga caa ggg gtg gta tat ttt 883
Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln Gly Val Val Tyr Phe
250 255 260

ctg ccc cta gga gtc att atc tct tca aat aaa gaa att ata gag atc 931
Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys Glu Ile Ile Glu Ile
265 270 275

agc aat cac tcc gca tcc tca att aac aca gca tca gga aaa cta tat 979
Ser Asn His Ser Ala Ser Ser Ile Asn Thr Ala Ser Gly Lys Leu Tyr
280 285 290

ccc ggt ggt ggc ggt atc atg tgt acc tcc ctt agt cat gag aac aat 1027
Pro Gly Gly Gly Gly Ile Met Cys Thr Ser Leu Ser His Glu Asn Asn
295 300 305

ccc aaa ggt ctt atc ttt aac aat aaa acg gca gca ctt agc ggc gga 1075
Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala Ala Leu Ser Gly Gly
310 315 320 325

gta tac aca cga gat ctt tca tct tcc aaa ata acg gtc cgc aca gca 1123
Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile Thr Val Arg Thr Ala
330 335 340

ttt att aat aac tct gcg act tca gga ggg gct ctc atc aat ctt tct 1171
Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala Leu Ile Asn Leu Ser
345 350 355

ggt ata gga agt act cct caa aat ttc ttc ctc tct gca gac tac ggc 1219
Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu Ser Ala Asp Tyr Gly
360 365 370

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gat att cta ttt aac aat aat aca atc aca tct tct tct cct caa ccc   1267
Asp Ile Leu Phe Asn Asn Asn Thr Ile Thr Ser Ser Ser Pro Gln Pro
    375                 380                 385

gga tat aga aat gca ctc tat gct gct ccg ggg att aac tta aaa cta   1315
Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly Ile Asn Leu Lys Leu
390                 395                 400                 405

gga gca aga cag ggt tat aaa att ctc ttt tat gat cct ata gat cac   1363
Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr Asp Pro Ile Asp His
                410                 415                 420

gat cag acg aca aca gat cct ata gta ttt aat tat gaa ccc cat cac   1411
Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn Tyr Glu Pro His His
            425                 430                 435

ctt ggc acc gtg ttg ttt tcc gga atc aat gta gat tct aac gca aca   1459
Leu Gly Thr Val Leu Phe Ser Gly Ile Asn Val Asp Ser Asn Ala Thr
        440                 445                 450

aat cca ttg aac ttc cta tca aaa ttt tct aac tct tca cga ctt gaa   1507
Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn Ser Ser Arg Leu Glu
    455                 460                 465

agg ggt gtg ctc gct att gaa gat cgg gct gct att tct tgc aaa acc   1555
Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala Ile Ser Cys Lys Thr
470                 475                 480                 485

cta tcg caa act ggg ggc att cta cgt tta gga aac gca gca tta atc   1603
Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly Asn Ala Ala Leu Ile
                490                 495                 500

agg acg aaa ggc ccg gga agc tcc ata aat ttt aat gca atc gcg atc   1651
Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe Asn Ala Ile Ala Ile
            505                 510                 515

aat ctt cct tct att tta caa tca gaa gcc tca gct cca aag ttc tgg   1699
Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser Ala Pro Lys Phe Trp
        520                 525                 530

att tat cct aca tta aca gga tcc acc tat tct gaa gac act tct tct   1747
Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser Glu Asp Thr Ser Ser
    535                 540                 545

act atc act ctc tca gga ccc ttg act ttt cta aac gat gaa aat gaa   1795
Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu Asn Asp Glu Asn Glu
550                 555                 560                 565

aac ccc tat gat agc tta gat ctc tct gaa cct cga aag gat atc ccc   1843
Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro Arg Lys Asp Ile Pro
                570                 575                 580

cct cct cta cct cct cga tgt gac tgc aaa aaa atc gat act tcg aat   1891
Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys Ile Asp Thr Ser Asn
            585                 590                 595
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ctc att gta gaa gcc atg aac tta gat gag cac tat gga tat cag gga 1939
Leu Ile Val Glu Ala Met Asn Leu Asp Glu His Tyr Gly Tyr Gln Gly
600 605 610

atc tgg tct ccc tat tgg atg gaa act acg act aca aca agc tct aca 1987
Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr Thr Thr Ser Ser Thr
615 620 625

gta ccg gaa cag acc aat aca aac cac agg cag ctc tac gta gac tgg 2035
Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln Leu Tyr Val Asp Trp
630 635 640 645

act cct gta gga tac cgc cct aac ccg gaa cgt cac gga gaa ttt att 2083
Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg His Gly Glu Phe Ile
650 655 660

gct aat acc tta tgg cag tct gcc tat aac gct ctg tta gga atc cgc 2131
Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala Leu Leu Gly Ile Arg
665 670 675

atc tta cct cca caa aac ctc aaa gag cat gac ctt gaa gcc tct ctg 2179
Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp Leu Glu Ala Ser Leu
680 685 690

caa gga ctc ggg ctt cta att aac caa cat aat cgc gag gga cgc aaa 2227
Gln Gly Leu Gly Leu Leu Ile Asn Gln His Asn Arg Glu Gly Arg Lys
695 700 705

ggc ttc cga aac cat act acg ggc tat gca gca aca acc tca gca aaa 2275
Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala Thr Thr Ser Ala Lys
710 715 720 725

act gca gca cga cat agt ttc tct tta gga ttc gca caa atg ttc tcc 2323
Thr Ala Ala Arg His Ser Phe Ser Leu Gly Phe Ala Gln Met Phe Ser
730 735 740

aaa act aga gaa cgt caa tct cca agt acg act tcc tcc cac aac tac 2371
Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr Ser Ser His Asn Tyr
745 750 755

ttt gca gga ctc cgc ttc gac agt ctc ctc ttc agg gac ttc atc tct 2419
Phe Ala Gly Leu Arg Phe Asp Ser Leu Leu Phe Arg Asp Phe Ile Ser
760 765 770

aca ggg cta tcc cta ggt tat agc tac gga gat cac cat atg ctt tgc 2467
Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp His His Met Leu Cys
775 780 785

cac tat aca gaa atc tta aaa ggg tcg tcc aaa gcc ttc ttt aat aac 2515
His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys Ala Phe Phe Asn Asn
790 795 800 805

cac act ttg gta gcc tct cta gac tgc aca ttc tta cca gct aga atc 2563
His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe Leu Pro Ala Arg Ile
810 815 820

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acc cgc act ctc gaa ctc cag ccc ttt atc agt gcc att gct ctg cgc   2611
Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser Ala Ile Ala Leu Arg
            825                 830                 835

tgt tcc cag gcc tcg ttc caa gaa act gga gac cat ata aga aaa ttc   2659
Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp His Ile Arg Lys Phe
        840                 845                 850

cat cca aaa cat ccc ctt aca gat ctt tcc tct ccc ata ggc ttc cgt   2707
His Pro Lys His Pro Leu Thr Asp Leu Ser Ser Pro Ile Gly Phe Arg
    855                 860                 865

tct gaa tgg aaa act tca cat cat atc ccc atg cta tgg act acg gaa   2755
Ser Glu Trp Lys Thr Ser His His Ile Pro Met Leu Trp Thr Thr Glu
870                 875                 880                 885

ata tcc tac gta cct acc cta tac aga aaa aat cca gaa atg ttc acg   2803
Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn Pro Glu Met Phe Thr
                890                 895                 900

aca cta ctc atc agc aat gga aca tgg aca aca caa gca act ccc gtc   2851
Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr Gln Ala Thr Pro Val
            905                 910                 915

tcc tat aat tcc gta gct gca aaa ata aaa aat act tcc caa ctt ttc   2899
Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn Thr Ser Gln Leu Phe
        920                 925                 930

tca aga gta acc tta tcc tta gat tat tca gct caa gtc tcc tcg tca   2947
Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala Gln Val Ser Ser Ser
    935                 940                 945

act gta ggt caa tac ctt aaa gct gag agt cat tgc aca ttt           2989
Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His Cys Thr Phe
950                 955                 960

taaccacaaa gaaaacatca aggaataaac agtgcaaaat aacagatccc ttagtaaatc 3049
ttccttcttt gttggagcct taattttagg taaaactaca ata                   3092
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attaaagttg cttcaacctt attgatttaa cgaggaaacc atg acc ata ctt cga   115
                                               Met Thr Ile Leu Arg
                                                 1               5
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aat ttt ctt acc tgc tcg gct tta ttc ctc gct ctc cct gca gca gca   163
Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala Leu Pro Ala Ala Ala
                 10                  15                  20

caa gtt gta tat ctt cat gaa agt gat ggt tat aac ggt gct atc aat   211
Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr Asn Gly Ala Ile Asn
             25                  30                  35

aat aaa agc tta gaa cct aaa att acc tgt tat cca gaa gga act tct   259
Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr Pro Glu Gly Thr Ser
         40                  45                  50

tac atc ttt cta gat gac gtg agg att tcc aac gtt aag cat gat caa   307
Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn Val Lys His Asp Gln
     55                  60                  65

gaa gat gct ggg gtt ttt ata aat cga tct ggg aat ctt ttt ttc atg   355
Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly Asn Leu Phe Phe Met
 70                  75                  80                  85

ggc aac cgt tgc aac ttc act ttt cac aac ctt atg acc gag ggt ttt   403
Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu Met Thr Glu Gly Phe
                 90                  95                 100

ggc gct gcc att tcg aac cgc gtt gga gac acc act ctc act ctc tct   451
Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr Thr Leu Thr Leu Ser
             105                 110                 115

aat ttt tct tac tta gcg ttc acc tca gca cct cta cta cct caa gga   499
Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro Leu Leu Pro Gln Gly
         120                 125                 130

caa gga gcg att tat agt ctt ggt tcc gtg atg atc gaa aat agt gag   547
Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met Ile Glu Asn Ser Glu
     135                 140                 145

gaa gtg act ttc tgt ggg aac tac tct tcg tgg agt gga gct gcg att   595
Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp Ser Gly Ala Ala Ile
150                 155                 160                 165

tat act ccc tac ctt tta ggt tct aag gcg agt cgt cct tca gta aat   643
Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser Arg Pro Ser Val Asn
                170                 175                 180

ctc agc ggg aac cgc tac ctg gtg ttt aga gac aat gtg agc caa gtt   691
Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp Asn Val Ser Gln Val
            185                 190                 195

tat ggc ggc gcc ata tct acc cac aat ctc aca ctc acg act cga gga   739
Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr Leu Thr Thr Arg Gly
        200                 205                 210

cct tcg tgt ttt gaa aat aat cat gct tat cat gac gtg aat agt aat   787
Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His Asp Val Asn Ser Asn
    215                 220                 225
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gga gga gcc att gcc att gct cct gga gga tcg atc tct ata tcc gtg   835
Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser Ile Ser Ile Ser Val
230                 235                 240                 245

aaa agc gga gat ctc atc ttc aaa gga aat aca gca tca caa gac gga   883
Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr Ala Ser Gln Asp Gly
                250                 255                 260

aat aca ata cac aac tcc atc cat ctg caa tct gga gca cag ttt aag   931
Asn Thr Ile His Asn Ser Ile His Leu Gln Ser Gly Ala Gln Phe Lys
            265                 270                 275

aac cta cgt gct gtt tca gaa tcc gga gtt tat ttc tat gat cct ata   979
Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr Phe Tyr Asp Pro Ile
        280                 285                 290

agc cat agc gag tcg cat aaa att aca gat ctt gta atc aat gct cct   1027
Ser His Ser Glu Ser His Lys Ile Thr Asp Leu Val Ile Asn Ala Pro
    295                 300                 305

gaa gga aag gaa act tat gaa gga aca att agc ttc tca gga cta tgc   1075
Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser Phe Ser Gly Leu Cys
310                 315                 320                 325

ctg gat gat cat gaa gtt tgt gcg gaa aat ctt act tcc aca atc cta   1123
Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu Thr Ser Thr Ile Leu
                330                 335                 340

caa gat gtc aca tta gca gga gga act ctc tct cta tcg gat ggg gtt   1171
Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser Leu Ser Asp Gly Val
            345                 350                 355

acc ttg caa ctg cat tct ttt aag cag gaa gca agc tct acg ctt act   1219
Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala Ser Ser Thr Leu Thr
        360                 365                 370

atg tct cca gga acc act ctg ctc tgc tca gga gat gct cgg gtt cag   1267
Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly Asp Ala Arg Val Gln
    375                 380                 385

aat ctg cac atc ctg att gaa gat acc gac aac ttt gtt cct gta agg   1315
Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn Phe Val Pro Val Arg
390                 395                 400                 405

att cgc gcc gag gac aag gat gct ctt gtc tca tta gaa aaa ctt aaa   1363
Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser Leu Glu Lys Leu Lys
                410                 415                 420

gtt gcc ttt gag gct tat tgg tcc gtc tat gac ttt cct caa ttt aag   1411
Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp Phe Pro Gln Phe Lys
            425                 430                 435

gaa gcc ttt acg att cct ctt ctt gaa ctt cta ggg cct tct ttt gac   1459
Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu Gly Pro Ser Phe Asp
        440                 445                 450
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agt ctt ctc cta ggg gag acc act ttg gag aga acc caa gtc aca aca   1507
Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg Thr Gln Val Thr Thr
    455                 460                 465

gag aat gac gcc gtt cga ggt ttc tgg tcc cta agc tgg gaa gag tac   1555
Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu Ser Trp Glu Glu Tyr
470                 475                 480                 485

ccc cct tct ctg gat aaa gac aga agg atc aca cca act aag aaa act   1603
Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr Pro Thr Lys Lys Thr
                490                 495                 500

gtt ttc ctc act tgg aat cct gag atc act tct acg cca taatctctaa    1652
Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser Thr Pro
            505                 510

gtctacacta taattaaggg aatccccttt aagaagattt tgggacctat ctgtattcag 1712
agataggtcc ctctatgcac acatgttcac gag                              1745
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<222> (101)..(967)

<400> 11

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                                            Met Gly Ile Ser Leu
                                              1               5

cca gag ctt ttt tcc aac cta ggt tct gct tac tta gat tat atc ttt   163
Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr Leu Asp Tyr Ile Phe
                10                  15                  20

caa cat cct ccg gcc tat gtt tgg tca gtt ttt ctt ctt tta tta gcc   211
Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe Leu Leu Leu Leu Ala
            25                  30                  35

cgt ctg ctt cct att ttt gct gta gct ccc ttc tta gga gca aag ctc   259
Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe Leu Gly Ala Lys Leu
        40                  45                  50

ttt ccc tcc cct att aaa atc ggg att agt ctc tct tgg ctt gca atc   307
Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu Ser Trp Leu Ala Ile
    55                  60                  65

atc ttt cca aaa gtc ttg gcg gat acg cag atc aca aat tac atg gat   355
Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile Thr Asn Tyr Met Asp
70                  75                  80                  85
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aac aat ctc ttt tat gtt tta ctt gtg aag gag atg atc ata ggc att 403
Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu Met Ile Ile Gly Ile
90 95 100

gtg ata ggc ttt gtt tta gca ttt ccc ttt tat gct gca caa tcg gca 451
Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr Ala Ala Gln Ser Ala
105 110 115

gga tct ttc atc act aac caa caa ggg att cag ggt tta gag ggc gcg 499
Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln Gly Leu Glu Gly Ala
120 125 130

aca tcc ctg att tcc att gag cag acc tct ccg cat ggc att tta tac 547
Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro His Gly Ile Leu Tyr
135 140 145

cat tac ttc gtg act att att ttt tgg tta gtg ggt ggt cac cgt att 595
His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val Gly Gly His Arg Ile
150 155 160 165

gta atc tct ttg tta ttg caa act ctt gaa gtc att ccg atc cat agt 643
Val Ile Ser Leu Leu Leu Gln Thr Leu Glu Val Ile Pro Ile His Ser
170 175 180

ttc ttt cct gcc gag atg atg agc tta agt gcc ccg att tgg att act 691
Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala Pro Ile Trp Ile Thr
185 190 195

atg atc aag atg tgc cag ctc tgt ctc gtg atg acc ata cag ctg agt 739
Met Ile Lys Met Cys Gln Leu Cys Leu Val Met Thr Ile Gln Leu Ser
200 205 210

gct cct gca gct ttg gcg atg tta atg tcc gac cta ttc tta ggg att 787
Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp Leu Phe Leu Gly Ile
215 220 225

att aac cgt atg gca cct caa gtt cag gtc atc tac ctc ctc tct gcc 835
Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile Tyr Leu Leu Ser Ala
230 235 240 245

ctt aag gct ttc atg ggt ctt ctc ttt ctc acc ctg gcg tgg tgg ttc 883
Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr Leu Ala Trp Trp Phe
250 255 260

ata att aag cag ata gat tat ttc act ctt gct tgg ttc aaa gaa gtc 931
Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala Trp Phe Lys Glu Val
265 270 275

ccc att atg ctc cta ggt tcc aac cct caa gta ctc taatccccta 977
Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val Leu
280 285

ggctcttatc gtgactctta tctggagatg cgctcactta cgaatcttag cgcactgttt 1037
atggattatc ttagggaatc tctcgcatat tcttttgtaa tctaagaatc tataaattca 1097
aga 1100

<210> 12
<211> 950
<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (101)..(895)

<400> 12
ccagtgataa agactctagt gataaagatg ctccagaagg aagcaatgaa attgagggtg 60

cttagtgact gccaacactt ttggaactct agacatcttg atg aag cac tcc aag 115
Met Lys His Ser Lys
1 5

gaa gat gac ctc tcc agg ttt ctt cct aaa aat ctt ctt gtt gaa tct 163
Glu Asp Asp Leu Ser Arg Phe Leu Pro Lys Asn Leu Leu Val Glu Ser
10 15 20

cct cat ccc gaa gaa atc cct tta aaa tct tta tct ttt acg atg agt 211
Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu Ser Phe Thr Met Ser
25 30 35

tgg cta cct aca att cat cct tca tgg att acc att gcc atg aaa gag 259
Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr Ile Ala Met Lys Glu
40 45 50

ttc cct cct gaa atc caa ggt caa tta tta gcg tgg ttg cca gag cct 307
Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala Trp Leu Pro Glu Pro
55 60 65

tta gtt caa gaa att cta ccc tta ctg cct ggc atc tct ata gcc cca 355
Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly Ile Ser Ile Ala Pro
70 75 80 85

cat cgc tgt gca cct ttc gga gcc ttc tat ctt cta gat atg cta agt 403
His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu Leu Asp Met Leu Ser
90 95 100

aaa aag atc cgt cct tgt gga att aca gaa gaa atc ttt ctt cct gca 451
Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu Ile Phe Leu Pro Ala
105 110 115

tcc tca gca aat gct ata ctt tac tat aca ggt cct gta aag atc gct 499
Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly Pro Val Lys Ile Ala
120 125 130

tta atc aac tgc cta ggt ctt tat tct att gct aaa gag ttg aag cac 547
Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala Lys Glu Leu Lys His
135 140 145

att ctg gat aag gtt gtg att gaa cga gtg aag aat gct ctc tcc cct 595
Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys Asn Ala Leu Ser Pro
150 155 160 165

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aca gag aaa ctc ttt ctt acc tac tgc caa tct cat ccg atg aaa cat   643
Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser His Pro Met Lys His
                170                 175                 180

tta gaa act acg aat ttt ctt tct tct tgg act act gat gca gaa tta   691
Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr Thr Asp Ala Glu Leu
            185                 190                 195

cga cag ttc gtt cat aag caa ggg tta gag ttt tta ggt aaa gca tta   739
Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe Leu Gly Lys Ala Leu
        200                 205                 210

aca aaa gaa aac gct tct ttt cta tgg tat ttt cta cgt agg tta gat   787
Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe Leu Arg Arg Leu Asp
    215                 220                 225

gtc ggt cga gca tat atc gtc gag cag act tta aaa aca tgg tat gac   835
Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu Lys Thr Trp Tyr Asp
230                 235                 240                 245

cat ccc tat gtg gat tat ttt aag tcc cgc cta gaa caa tgc atg aaa   883
His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu Glu Gln Cys Met Lys
                250                 255                 260

gtc tta gtg aaa taaaagcttt ataagtaaag atttagcttt atacaaagta       935
Val Leu Val Lys
            265

tagaaaaata acacg                                                 950
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<210> 13
<211> 500
<212> DNA
<213> Chlamydia pneumoniae

<220>
<221> CDS
<222> (101)..(385)

<400> 13

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cgatttcgtt acctttaaag ttacttttga tcgtcatggt agacggatgg acattactgc 60

tccaagggct tatgatcagc tttaaataag gacacgtgcc atg tta gca ttt ttc   115
                                            Met Leu Ala Phe Phe
                                              1               5

gca act agt ttc aaa tct gtt ctt ttt gag tac tcc tac caa tca tta   163
Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr Ser Tyr Gln Ser Leu
            10                  15                  20

tta ctt att ttg att gtt tcg gca cct ccc atc atc tta gct tcc ata   211
Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile Ile Leu Ala Ser Ile
        25                  30                  35

gtc ggg att atg gtt gcg atc ttc caa gcc gca aca caa atc caa gaa   259
Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala Thr Gln Ile Gln Glu
    40                  45                  50
```

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cag acc ttc gct ttt gca gtc aaa cta gtc gtg att ttt gga acc tta   307
Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val Ile Phe Gly Thr Leu
     55                  60                  65

atg atc tct gga ggg tgg ctt agc aat atg att tta cgc ttt gca ggt   355
Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile Leu Arg Phe Ala Gly
 70                  75                  80                  85

cag att ttc caa aac ttc tat aaa tgg aaa taaagagctt atgggaatct     405
Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys
                 90                  95

ctctaccaga gctttttcc aacctaggtt ctgcttactt agattatatc tttcaacatc 465
ctccggccta tgtttggtca gtttttcttc tttta                           500
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<210> 14
<211> 552
<212> PRT
<213> Chlamydia pneumoniae

<400> 14

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Met Val Ser Ser Pro Ile Leu Asn Val Pro Leu Lys Asn His Ala Ser
  1               5                  10                  15

Val Ser Gly Lys Phe Thr His Arg Glu Val Ser Lys Leu Ala Ser Asp
             20                  25                  30

Leu Lys Ser Gly Ala Met Ser Phe Val Pro Glu Val Leu Ser Glu Glu
         35                  40                  45

Thr Ile Ser Ser Asp Leu Gly Lys Lys Gln Cys Thr Gln Gly Ile Ile
     50                  55                  60

Ser Ala Cys Cys Gly Leu Ala Met Leu Ile Val Leu Met Ser Val Tyr
 65                  70                  75                  80

Tyr Arg Phe Gly Gly Val Ile Ala Ser Gly Ala Val Leu Leu Asn Leu
                 85                  90                  95

Leu Leu Ile Trp Ala Ala Leu Gln Tyr Leu Asp Ala Pro Leu Thr Leu
            100                 105                 110

Ser Gly Leu Ala Gly Ile Val Leu Ala Met Gly Met Ala Val Asp Ala
        115                 120                 125

Asn Val Leu Val Phe Glu Arg Ile Arg Glu Glu Phe Leu Leu Ser Gln
    130                 135                 140

Ser Leu Lys Lys Ser Val Glu Lys Gly Tyr Thr Lys Ala Phe Gly Ala
145                 150                 155                 160

Ile Phe Asp Ser Asn Leu Thr Thr Val Leu Ala Ser Ala Leu Leu Phe
                165                 170                 175

Phe Leu Asp Thr Gly Pro Ile Lys Gly Phe Ala Leu Thr Leu Ile Leu
            180                 185                 190
```

Gly Ile Phe Ser Ser Met Phe Thr Ala Leu Phe Met Thr Lys Phe Phe
195 200 205

Phe Met Leu Trp Met Asn Lys Thr Gln His Thr Gln Leu His Met Met
210 215 220

Asn Lys Phe Val Gly Ile Lys His Asp Phe Leu Arg Gly Cys Lys Lys
225 230 235 240

Leu Trp Ala Val Ser Gly Ser Val Phe Leu Leu Gly Cys Val Ala Leu
245 250 255

Gly Phe Gly Ala Trp Asn Ser Val Leu Gly Met Asp Phe Lys Gly Gly
260 265 270

Tyr Ala Phe Thr Phe Asn Pro Lys Glu His Gly Ile Ser Asp Val Ala
275 280 285

Gln Met Arg Gly Lys Val Val His Lys Leu Gln Glu Ala Gly Leu Ser
290 295 300

Ser Arg Asp Phe Arg Ile Gln Thr Phe Gly Ser Ser Glu Lys Ile Lys
305 310 315 320

Ile Tyr Phe Ser Asp Lys Ala Leu Ser Tyr Thr Lys Gln Ile Arg Ala
325 330 335

Ser Leu Leu Lys Leu Thr Ile Met Ser Trp Arg Tyr Cys Gly Ile Val
340 345 350

Val Arg Asn Arg Pro Arg Phe Leu Tyr Gly Asn Ser Lys Arg Asn Ala
355 360 365

Lys Phe Trp Ser Lys Val Ser Ser Lys Leu Ser Lys Lys Met Arg Tyr
370 375 380

Gln Ala Thr Ile Gly Leu Leu Gly Ala Leu Ala Ile Ile Leu Leu Tyr
385 390 395 400

Val Ser Leu Arg Phe Glu Trp Gln Tyr Ala Phe Ser Ala Val Cys Ala
405 410 415

Leu Ile His Asp Leu Leu Ala Thr Cys Ala Val Leu Phe Ile Ala His
420 425 430

Phe Phe Leu Lys Lys Ile Gln Ile Asp Leu Gln Ala Ile Gly Ala Leu
435 440 445

Met Thr Val Leu Gly Tyr Ser Leu Asn Asn Thr Leu Ile Ile Phe Asp
450 455 460

Arg Ile Arg Glu Asp Arg Gln Ala Asn Leu Phe Thr Pro Met His Val
465 470 475 480

Leu Val Asn Asp Ala Leu Gln Lys Thr Phe Ser Arg Thr Val Met Thr
485 490 495

Thr Ala Thr Thr Leu Ser Val Leu Leu Met Leu Leu Phe Ile Gly Gly
500 505 510

Ser Ser Val Phe Asn Phe Ala Phe Ile Met Thr Ile Gly Ile Leu Leu
515 520 525

Gly Thr Leu Ser Ser Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met
530 535 540

Val Arg Lys Glu Asn Arg Ser Lys
545 550

<210> 15
<211> 196
<212> PRT
<213> Chlamydia pneumoniae

<400> 15
Met Ser Ser Asn Leu His Pro Val Gly Gly Thr Gly Thr Gly Ala Ala
1 5 10 15

Ala Pro Glu Ser Val Leu Asn Ile Val Glu Glu Ile Ala Ala Ser Gly
20 25 30

Ser Val Thr Ala Gly Leu Gln Ala Ile Thr Ser Ser Pro Gly Met Val
35 40 45

Asn Leu Leu Ile Gly Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg
50 55 60

Glu Ser Lys Leu Phe Gln Ser Arg Ala Cys Gln Ile Thr Leu Leu Val
65 70 75 80

Leu Gly Ile Leu Leu Val Val Ala Gly Leu Ala Cys Met Phe Ile Phe
85 90 95

His Ser Gln Leu Gly Ala Asn Ala Phe Trp Leu Ile Ile Pro Ala Ala
100 105 110

Ile Gly Leu Ile Lys Leu Leu Val Thr Ser Leu Cys Phe Asp Glu Ala
115 120 125

Cys Thr Ser Glu Lys Leu Met Val Phe Gln Lys Trp Ala Gly Val Leu
130 135 140

Glu Asp Gln Leu Asp Asp Gly Ile Leu Asn Asn Ser Asn Lys Ile Phe
145 150 155 160

Gly His Val Lys Thr Glu Gly Asn Thr Ser Arg Ala Thr Thr Pro Val
165 170 175

Leu Asn Asp Gly Arg Gly Thr Pro Val Leu Ser Pro Leu Val Ser Lys
180 185 190

Ile Ala Arg Val
195

<210> 16
<211> 245
<212> PRT
<213> Chlamydia pneumoniae

<400> 16
Met Thr Ile Arg Ile Leu Ala Glu Gly Leu Ala Phe Arg Tyr Gly Ser
1 5 10 15

Lys Gly Pro Asn Ile Ile His Asp Val Ser Phe Ser Val Tyr Asp Gly
20 25 30

Asp Phe Ile Gly Ile Ile Gly Pro Asn Gly Gly Gly Lys Ser Thr Leu
35 40 45

Thr Met Leu Ile Leu Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys
50 55 60

Thr Phe Pro Ser His Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly
65 70 75 80

Trp Val Pro Gln His Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val
85 90 95

Lys Asp Val Val Leu Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly
100 105 110

Lys Tyr Lys Lys Lys Asp Phe Glu Ala Val Asp His Ala Leu Asp Leu
115 120 125

Val Gly Leu Ser Asp Thr Thr Thr Thr Ala Phe Ala His Leu Ser Gly
130 135 140

Gly Gln Ile Gln Arg Val Leu Leu Ala Arg Ala Leu Ala Ser Tyr Pro
145 150 155 160

Glu Ile Leu Ile Leu Asp Glu Pro Thr Thr Asn Ile Asp Pro Asp Asn
165 170 175

Gln Gln Arg Ile Leu Ser Ile Leu Lys Lys Leu Asn Arg Thr Cys Thr
180 185 190

Ile Leu Met Val Thr His Asp Leu His His Thr Thr Asn Tyr Phe Asn
195 200 205

Lys Val Phe Tyr Met Asn Lys Thr Leu His Phe Ile Gly Arg His Phe
210 215 220

Asp Leu Asn Arg Pro Ile Leu Leu Ser Ser Tyr Lys Asn Gln Glu Phe
225 230 235 240

Ser Cys Ser Pro His
245

<210> 17
<211> 278

<212> PRT
<213> Chlamydia pneumoniae

<400> 17

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Met His Lys Val Ile Val Phe Ile Phe Leu Thr Leu Tyr Ser Leu Lys
 1               5                  10                  15

Ser Tyr Gly Asn Asp Val Ile Asp Lys Pro His Val Leu Val Ser Ile
            20                  25                  30

Ala Pro Tyr Lys Phe Leu Val Glu Gln Ile Ala Glu Glu Thr Cys Phe
        35                  40                  45

Val Tyr Ala Ile Val Thr Asn His Tyr Asp Pro His Thr Tyr Glu Leu
    50                  55                  60

Pro Pro Gln Gln Ile Lys Glu Leu Arg Gln Gly Asp Leu Trp Phe Arg
65                  70                  75                  80

Ile Gly Glu Ala Phe Gly Lys Asn Leu Leu Glu Lys Pro Tyr Met Gln
                85                  90                  95

Gln Val Asp Leu Ser Gln Asn Val Ser Leu Ile Gln Gly Lys Pro Cys
            100                 105                 110

Cys Asn Gln His Thr Thr Asn Tyr Asp Thr His Thr Trp Leu Ser Pro
        115                 120                 125

Lys Asn Leu Lys Val Gln Val Glu Thr Ile Val Thr Thr Leu Ser Lys
    130                 135                 140

Lys Tyr Pro Gln His Ala Thr Leu Tyr Gln Ser Asn Gly Glu Lys Leu
145                 150                 155                 160

Leu Leu Ala Leu Asp Gln Leu Asn Glu Glu Ile Leu Thr Ile Thr Ser
                165                 170                 175

Lys Ala Lys Gln Arg His Ile Leu Val Ser His Gly Ala Phe Gly Tyr
            180                 185                 190

Phe Cys Arg Asp Tyr Asn Phe Ser Gln His Thr Ile Glu Lys Ser Ser
        195                 200                 205

His Val Glu Pro Ser Pro Lys Asp Val Ala Arg Val Phe Arg Asp Ile
    210                 215                 220

Glu Gln Tyr Lys Ile Ser Ser Val Ile Leu Leu Glu Tyr Ser Gly Arg
225                 230                 235                 240

Arg Ser Ser Ala Met Leu Ala Asp Arg Phe His Met His Thr Val Asn
                245                 250                 255

Leu Asp Pro Tyr Ala Glu Asn Val Leu Val Asn Leu Lys Thr Ile Ala
            260                 265                 270

Thr Thr Phe Ser Ser Leu
        275
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<210> 18
<211> 469
<212> PRT
<213> Chlamydia pneumoniae

<400> 18

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Met Gly Pro Gly Ser Val Leu Ser Asn His Ser Lys Glu Ala Gly Gly
 1               5                  10                  15

Ile Ala Ile Asn Asn Val Ile Ile Asp Phe Ser Glu Ile Val Pro Thr
            20                  25                  30

Lys Asp Asn Ala Thr Val Ala Pro Pro Thr Leu Lys Leu Val Ser Arg
        35                  40                  45

Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp Ile Thr Gly Thr Val Thr
    50                  55                  60

Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln Asn Ser Tyr Leu Gly Glu
65                  70                  75                  80

Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp Asn Ser Ala Ser Gly Ala
                85                  90                  95

Val Thr Ala Thr Asn Val Thr Leu Gln Gly Asn Leu Gly Ala Lys Lys
            100                 105                 110

Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro Asn Ser Ser Gly Ser Lys
        115                 120                 125

Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr Leu Arg Trp Pro Tyr Ile
    130                 135                 140

Pro Arg Asp Asn His Phe Tyr Ile Asn Ser Ile Trp Gly Ala Gln Asn
145                 150                 155                 160

Ser Leu Val Thr Val Asn Gln Gly Ile Leu Gly Asn Met Leu Asn Asn
                165                 170                 175

Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn Phe Trp Ala Ser Ala Ile
            180                 185                 190

Gly Ser Phe Leu Arg Lys Glu Val Ser Arg Asn Ser Asp Ser Phe Thr
        195                 200                 205

Tyr His Gly Arg Gly Tyr Thr Ala Ala Val Asp Ala Lys Pro Arg Gln
    210                 215                 220

Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln Val Phe Gly His Ala Glu
225                 230                 235                 240

Ser Glu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly His Ser
                245                 250                 255

Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile Phe Tyr Phe Pro Ala Ile
            260                 265                 270
```

Arg Ser Arg Pro Ile Leu Phe Gln Gly Val Ala Thr Tyr Gly Tyr Met
275 280 285

Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser Ile Glu Glu Lys Asn Met
290 295 300

Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe Asp Leu Arg Phe Ser Val
305 310 315 320

Asp Leu Lys Glu Pro Gln Pro His Ser Thr Ala Arg Leu Thr Phe Tyr
325 330 335

Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln Glu Lys Phe Thr Glu Leu
340 345 350

Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys Ser Tyr Gly Asn Leu Ala
355 360 365

Ile Pro Thr Gly Phe Ser Val Asp Gly Ala Leu Ala Trp Arg Glu Ile
370 375 380

Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr Leu Pro Val Ile Leu Arg
385 390 395 400

Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu Ser Thr Lys Glu Lys Gly
405 410 415

Asn Val Val Asn Val Leu Pro Thr Arg Asn Ala Ala Arg Ala Glu Val
420 425 430

Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp Thr Leu Tyr Gly Thr Tyr
435 440 445

Thr Ile Asp Ala Ser Met Asn Thr Leu Val Gln Met Ala Asn Gly Gly
450 455 460

Ile Arg Phe Val Phe
465

<210> 19
<211> 922
<212> PRT
<213> Chlamydia pneumoniae

<400> 19
Met Arg Phe Ser Leu Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu
1 5 10 15

Leu Ser Val Phe Asp Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr
20 25 30

Pro Glu Asp Ser Phe His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr
35 40 45

Asn Val Gln Ala Gly Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile
50 55 60

Ser Asn Val Asp Asn Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr
65 70 75 80

Ser Gly Ser Val Thr Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn
85 90 95

Asn Ile Ser Ser Gly Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln
100 105 110

Asp Pro Gln Ala Thr Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe
115 120 125

Ile Gln Ser Pro Gly Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys
130 135 140

Asn Ala Leu Met Leu Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn
145 150 155 160

Gln Ser Lys Thr Lys Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile
165 170 175

Val Gly Asn Tyr Asp Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe
180 185 190

Gly Gly Ala Ile His Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln
195 200 205

Ala Glu Ile Arg Phe Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly
210 215 220

Ala Leu Tyr Ser Asp Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val
225 230 235 240

Leu Phe Arg Glu Asn Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly
245 250 255

Ala Val Cys Cys Leu Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile
260 265 270

Val Thr Phe Ser Asp Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser
275 280 285

Ile Met Gly Gly Gly Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser
290 295 300

Gly Gly Pro Thr Leu Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln
305 310 315 320

Asn Leu Gly Gly Ala Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu
325 330 335

Ser Ala Glu Lys Gly Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu
340 345 350

Pro Phe Leu Asn Gly Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys
355 360 365

Leu Gln Ala Arg Asn Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr
370 375 380

Ser Glu Ala Asp Gly Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys
385 390 395 400

Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu
405 410 415

Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn
420 425 430

Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val
435 440 445

Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly
450 455 460

Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala
465 470 475 480

Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys
485 490 495

Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu
500 505 510

Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser
515 520 525

Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val
530 535 540

Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe
545 550 555 560

Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly
565 570 575

Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu
580 585 590

Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg
595 600 605

Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp
610 615 620

Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala
625 630 635 640

Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu
645 650 655

Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe
660 665 670

Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu
675 680 685

Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu
690 695 700

Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly
705 710 715 720

Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe
725 730 735

Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala
740 745 750

Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile
755 760 765

Glu Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu
770 775 780

Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr
785 790 795 800

His Gly Asp Phe Lys Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn
805 810 815

Gly Ser Leu Thr Ser Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys
820 825 830

Leu Ala Leu Ser Gln Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile
835 840 845

Pro Asp Ile Phe Arg Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile
850 855 860

Ser Gly Asp Ser Trp Leu Val Pro Ala Ala His Val Ser Arg His Ala
865 870 875 880

Phe Val Gly Ser Gly Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu
885 890 895

Leu Leu Cys Arg Gly Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr
900 905 910

Asn Ile Asn Cys Gly Ser Lys Phe Arg Phe
915 920

<210> 20
<211> 375
<212> PRT
<213> Chlamydia pneumoniae

<400> 20
Met Pro Ser Ser Trp Lys Arg Leu Leu Gln Val Leu Ser His Lys Ile
1 5 10 15

Ala Ala Thr Glu Ser Gly Gly Gly Ile Tyr Ala Lys Asp Ile Gln Leu
20 25 30

Gln Ala Leu Pro Gly Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr
35 40 45

Ser Leu Thr Thr Ser Thr Asn Leu Tyr Gly Gly Gly Ile Tyr Ser Ser
50 55 60

Gly Ala Val Thr Leu Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly
65 70 75 80

Asn Ser Val Ile Asn Thr Ala Thr Ser Gln Asp Ala Asp Ile Gln Gly
85 90 95

Gly Gly Ile Tyr Ala Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr
100 105 110

Pro Ile Leu Phe Ser Asn Asn Ser Ala Ala Thr Lys Lys Thr Ser Thr
115 120 125

Thr Lys Gln Ile Ala Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile
130 135 140

Glu Asn Asn Ser Gln Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser
145 150 155 160

Glu Ala Thr Thr Ala Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly
165 170 175

Ala Ile Ala Ala Asn Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr
180 185 190

Phe Lys Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp
195 200 205

Leu Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly
210 215 220

Ser Val Leu Phe Gln Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile
225 230 235 240

Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly
245 250 255

Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu
260 265 270

Thr Leu Ala Pro Asn Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr
275 280 285

Glu Thr Thr Ala Thr Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala
290 295 300

Ile Tyr Gly Asn Asn Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala
305 310 315 320

Glu Asn Gly Ser Ile Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn
325 330 335

Lys Tyr Cys Ser Ile Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala
340 345 350

Ser Ala Gly Lys Ala Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro
355 360 365

Lys Lys Gln Leu Leu Lys Ser
370 375

<210> 21
<211> 871
<212> PRT
<213> Chlamydia pneumoniae

<400> 21
Met Lys Tyr Ser Leu Pro Trp Leu Leu Thr Ser Ser Ala Leu Val Phe
1 5 10 15

Ser Leu His Pro Leu Met Ala Ala Asn Thr Asp Leu Ser Ser Ser Asp
20 25 30

Asn Tyr Glu Asn Gly Ser Ser Gly Ser Ala Ala Phe Thr Ala Lys Glu
35 40 45

Thr Ser Asp Ala Ser Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser
50 55 60

Ile Thr Asn Val Ser Ala Ile Thr Pro Ala Asp Lys Ser Cys Phe Thr
65 70 75 80

Asn Thr Gly Gly Ala Leu Ser Phe Val Gly Ala Asp His Ser Leu Val
85 90 95

Leu Gln Thr Ile Ala Leu Thr His Asp Gly Ala Ala Ile Asn Asn Thr
100 105 110

Asn Thr Ala Leu Ser Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser
115 120 125

Ala Pro Ala Thr Gly Thr Ser Gly Gly Lys Gly Ala Ile Cys Val Thr
130 135 140

Asn Thr Glu Gly Gly Thr Ala Thr Phe Thr Asp Asn Ala Ser Val Thr
145 150 155 160

Leu Gln Lys Asn Thr Ser Glu Lys Asp Gly Ala Ala Val Ser Ala Tyr
165 170 175

Ser Ile Asp Leu Ala Lys Thr Thr Thr Ala Ala Leu Leu Asp Gln Asn
180 185 190

Thr Ser Thr Lys Asn Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr
195 200 205

Val Gln Gly Asn Ser Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr
210 215 220

Asp Lys Gly Gly Gly Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp
225 230 235 240

Ala Asn Thr Gly Val Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly
245 250 255

Gly Ala Trp Ser Ser Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln
260 265 270

Val Leu Phe Gln Glu Asn Lys Thr Thr Gly Ser Ala Ala Gln Ala Asn
275 280 285

Asn Pro Glu Gly Cys Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala
290 295 300

Thr Asp Lys Thr Gly Leu Ala Ile Ser Gln Asn Gln Glu Met Ser Phe
305 310 315 320

Thr Ser Asn Thr Thr Thr Ala Asn Gly Gly Ala Ile Tyr Ala Thr Lys
325 330 335

Cys Thr Leu Asp Gly Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala
340 345 350

Thr Ala Gly Cys Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser
355 360 365

Leu Lys Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys
370 375 380

Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn
385 390 395 400

Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser
405 410 415

Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ala Phe Ile Asp
420 425 430

Ser Gly Ser Val Ser Asp Lys Thr Gly Leu Ser Ile Ala Asn Asn Gln
435 440 445

Glu Val Ser Leu Thr Ser Asn Ala Ala Thr Val Ser Gly Gly Ala Ile
450 455 460

Tyr Ala Thr Lys Cys Thr Leu Thr Gly Asn Gly Ser Leu Thr Phe Asp
465 470 475 480

Gly Asn Thr Ala Gly Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu
485 490 495

Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn
500 505 510

Thr Ala Lys Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu
515 520 525

Ser Gly Asn Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro
530 535 540

Ser Asn Ser Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser
545 550 555 560

Phe Leu Glu Ser Ala Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu
565 570 575

Asp Asn Glu Asn Val Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly
580 585 590

Gly Ala Ile Tyr Ala Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu
595 600 605

Thr Phe Asp Gly Asn Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr
610 615 620

Glu Thr Glu Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe
625 630 635 640

Ser Thr Asn Thr Ala Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn
645 650 655

Thr Ser Phe Thr Lys Asn Lys Ala Leu Val Phe Ser Gly Asn Ser Ala
660 665 670

Thr Ala Thr Ala Thr Thr Thr Thr Asp Gln Glu Gly Cys Gly Gly Ala
675 680 685

Ile Leu Cys Asn Ile Ser Glu Ser Asp Ile Ala Thr Lys Ser Leu Thr
690 695 700

Leu Thr Glu Asn Glu Ser Leu Ser Phe Ile Asn Asn Thr Ala Lys Arg
705 710 715 720

Ser Gly Gly Gly Ile Tyr Ala Pro Lys Cys Val Ile Ser Gly Ser Glu
725 730 735

Ser Ile Asn Phe Asp Gly Asn Thr Ala Glu Thr Ser Gly Gly Ala Ile
740 745 750

Tyr Ser Lys Asn Leu Ser Ile Thr Ala Asn Gly Pro Val Ser Phe Thr
755 760 765

Asn Asn Ser Gly Gly Lys Gly Gly Ala Ile Tyr Ile Ala Asp Ser Gly
770 775 780

Glu Leu Ser Leu Glu Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn
785 790 795 800

Arg Ala Thr Glu Gly Thr Ser Thr Pro Asn Ser Ile His Leu Gly Ala
805 810 815

Arg Gly Lys Ile Thr Lys Leu Ala Ala Ala Pro Gly His Thr Ile Tyr
820 825 830

Phe Tyr Asp Pro Ile Thr Met Glu Ala Pro Ala Ser Gly Gly Thr Ile
835 840 845

Glu Glu Leu Val Ile Asn Pro Val Val Lys Ala Ile Val Pro Pro Pro
850 855 860

Gln Pro Lys Asn Gly Pro Ile
865 870

<210> 22
<211> 963
<212> PRT
<213> Chlamydia pneumoniae

<400> 22
Met Thr Asn Ser Ile Phe Ile Ser Lys Phe Gly Cys Leu Cys Asp Pro
1 5 10 15

Phe Val Ser Ala Phe Tyr Pro Thr Ala Leu Cys Cys Ser Leu Ser Gly
20 25 30

Asn Glu Val Pro Asn Leu Ala Ser Cys Gln Met Ser Arg Lys Asp Ile
35 40 45

Ser Ala Phe His Thr Ser Pro Ser Phe Arg Leu Asn Val Thr Pro Glu
50 55 60

Pro Leu Val Ser Ser Phe Arg Pro Ser Asn Leu Leu Asn Gly Phe Gly
65 70 75 80

His Asp Ile Thr Gln Asp Ile Thr Ile Thr Gly Asn Ser Ile Asn Ser
85 90 95

Val Ile Asp Tyr Asn Tyr His Tyr Glu Asp Gly Gly Ile Leu Ala Cys
100 105 110

Lys Asn Leu Phe Ile Ser Glu Asn Lys Gly Asn Leu Ser Phe Glu Arg
115 120 125

Asn Ser Ser His Ser Ser Gly Gly Ala Leu Tyr Ser Val Arg Glu Cys
130 135 140

Trp Ile Ser Lys Asn Gln Asn Tyr Ser Phe Ile Ser Asn Ala Ala Ser
145 150 155 160

Leu Ala Thr Thr Thr Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu
165 170 175

Asp Ser Tyr Ile Thr Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn
180 185 190

Val Ser Lys Asn Arg Gly Gly Ala Ile Tyr Val Gly Val Ser Leu Ser
195 200 205

Ile Thr Asp Asn Leu Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu
210 215 220

Glu Asp Ser Ser Phe Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile
225 230 235 240

Glu Arg Asn Tyr Gln Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln
245 250 255

Gly Val Val Tyr Phe Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys
260 265 270

Glu Ile Ile Glu Ile Ser Asn His Ser Ala Ser Ser Ile Asn Thr Ala
275 280 285

Ser Gly Lys Leu Tyr Pro Gly Gly Gly Gly Ile Met Cys Thr Ser Leu
290 295 300

Ser His Glu Asn Asn Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala
305 310 315 320

Ala Leu Ser Gly Gly Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile
325 330 335

Thr Val Arg Thr Ala Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala
340 345 350

Leu Ile Asn Leu Ser Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu
355 360 365

Ser Ala Asp Tyr Gly Asp Ile Leu Phe Asn Asn Asn Thr Ile Thr Ser
370 375 380

Ser Ser Pro Gln Pro Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly
385 390 395 400

Ile Asn Leu Lys Leu Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr
405 410 415

Asp Pro Ile Asp His Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn
420 425 430

Tyr Glu Pro His His Leu Gly Thr Val Leu Phe Ser Gly Ile Asn Val
435 440 445

Asp Ser Asn Ala Thr Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn
450 455 460

Ser Ser Arg Leu Glu Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala
465 470 475 480

Ile Ser Cys Lys Thr Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly
485 490 495

Asn Ala Ala Leu Ile Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe
500 505 510

Asn Ala Ile Ala Ile Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser
515 520 525

Ala Pro Lys Phe Trp Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser
530 535 540

Glu Asp Thr Ser Ser Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu
545 550 555 560

Asn Asp Glu Asn Glu Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro
565 570 575

Arg Lys Asp Ile Pro Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys
580 585 590

Ile Asp Thr Ser Asn Leu Ile Val Glu Ala Met Asn Leu Asp Glu His
595 600 605

Tyr Gly Tyr Gln Gly Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr
610 615 620

Thr Thr Ser Ser Thr Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln
625 630 635 640

Leu Tyr Val Asp Trp Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg
645 650 655

His Gly Glu Phe Ile Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala
660 665 670

Leu Leu Gly Ile Arg Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp
675 680 685

Leu Glu Ala Ser Leu Gln Gly Leu Gly Leu Leu Ile Asn Gln His Asn
690 695 700

Arg Glu Gly Arg Lys Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala
705 710 715 720

Thr Thr Ser Ala Lys Thr Ala Ala Arg His Ser Phe Ser Leu Gly Phe
725 730 735

Ala Gln Met Phe Ser Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr
740 745 750

Ser Ser His Asn Tyr Phe Ala Gly Leu Arg Phe Asp Ser Leu Leu Phe
755 760 765

Arg Asp Phe Ile Ser Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp
770 775 780

His His Met Leu Cys His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys
785 790 795 800

Ala Phe Phe Asn Asn His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe
805 810 815

Leu Pro Ala Arg Ile Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser
820 825 830

Ala Ile Ala Leu Arg Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp
835 840 845

His Ile Arg Lys Phe His Pro Lys His Pro Leu Thr Asp Leu Ser Ser
850 855 860

Pro Ile Gly Phe Arg Ser Glu Trp Lys Thr Ser His His Ile Pro Met
865 870 875 880

Leu Trp Thr Thr Glu Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn
885 890 895

Pro Glu Met Phe Thr Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr
900 905 910

Gln Ala Thr Pro Val Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn
915 920 925

Thr Ser Gln Leu Phe Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala
930 935 940

Gln Val Ser Ser Ser Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His
945 950 955 960

Cys Thr Phe

<210> 23
<211> 514
<212> PRT
<213> Chlamydia pneumoniae

<400> 23
Met Thr Ile Leu Arg Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala
1 5 10 15

Leu Pro Ala Ala Ala Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr
20 25 30

Asn Gly Ala Ile Asn Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr
35 40 45

Pro Glu Gly Thr Ser Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn
50 55 60

Val Lys His Asp Gln Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly
65 70 75 80

Asn Leu Phe Phe Met Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu
85 90 95

Met Thr Glu Gly Phe Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr
100 105 110

Thr Leu Thr Leu Ser Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro
115 120 125

Leu Leu Pro Gln Gly Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met
130 135 140

Ile Glu Asn Ser Glu Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp
145 150 155 160

Ser Gly Ala Ala Ile Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser
165 170 175

Arg Pro Ser Val Asn Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp
180 185 190

Asn Val Ser Gln Val Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr
195 200 205

Leu Thr Thr Arg Gly Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His
210 215 220

Asp Val Asn Ser Asn Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser
225 230 235 240

Ile Ser Ile Ser Val Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr
245 250 255

Ala Ser Gln Asp Gly Asn Thr Ile His Asn Ser Ile His Leu Gln Ser
260 265 270

Gly Ala Gln Phe Lys Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr
275 280 285

Phe Tyr Asp Pro Ile Ser His Ser Glu Ser His Lys Ile Thr Asp Leu
290 295 300

Val Ile Asn Ala Pro Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser
305 310 315 320

Phe Ser Gly Leu Cys Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu
325 330 335

Thr Ser Thr Ile Leu Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser
340 345 350

Leu Ser Asp Gly Val Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala
355 360 365

Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly
370 375 380

Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn
385 390 395 400

Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser
405 410 415

Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp
420 425 430

Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu
435 440 445

Gly Pro Ser Phe Asp Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg
450 455 460

Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu
465 470 475 480

Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr
485 490 495

Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser
500 505 510

Thr Pro

<210> 24
<211> 289
<212> PRT
<213> Chlamydia pneumoniae

<400> 24
Met Gly Ile Ser Leu Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr
1 5 10 15

Leu Asp Tyr Ile Phe Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe
20 25 30

Leu Leu Leu Leu Ala Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe
35 40 45

Leu Gly Ala Lys Leu Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu
50 55 60

Ser Trp Leu Ala Ile Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile
65 70 75 80

Thr Asn Tyr Met Asp Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu
85 90 95

Met Ile Ile Gly Ile Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr
100 105 110

Ala Ala Gln Ser Ala Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln
115 120 125

Gly Leu Glu Gly Ala Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro
130 135 140

His Gly Ile Leu Tyr His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val
145 150 155 160

Gly Gly His Arg Ile Val Ile Ser Leu Leu Leu Gln Thr Leu Glu Val
165 170 175

Ile Pro Ile His Ser Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala
180 185 190

Pro Ile Trp Ile Thr Met Ile Lys Met Cys Gln Leu Cys Leu Val Met
195 200 205

Thr Ile Gln Leu Ser Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp
210 215 220

Leu Phe Leu Gly Ile Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile
225 230 235 240

Tyr Leu Leu Ser Ala Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr
245 250 255

Leu Ala Trp Trp Phe Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala
260 265 270

Trp Phe Lys Glu Val Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val
275 280 285

Leu

<210> 25
<211> 265
<212> PRT
<213> Chlamydia pneumoniae

<400> 25
Met Lys His Ser Lys Glu Asp Asp Leu Ser Arg Phe Leu Pro Lys Asn
1 5 10 15

Leu Leu Val Glu Ser Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu
20 25 30

Ser Phe Thr Met Ser Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr
35 40 45

Ile Ala Met Lys Glu Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala
50 55 60

Trp Leu Pro Glu Pro Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly
65 70 75 80

Ile Ser Ile Ala Pro His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu
85 90 95

Leu Asp Met Leu Ser Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu
100 105 110

Ile Phe Leu Pro Ala Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly
115 120 125

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Pro Val Lys Ile Ala Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala
    130                 135                 140

Lys Glu Leu Lys His Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys
145                 150                 155                 160

Asn Ala Leu Ser Pro Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser
                165                 170                 175

His Pro Met Lys His Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr
            180                 185                 190

Thr Asp Ala Glu Leu Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe
        195                 200                 205

Leu Gly Lys Ala Leu Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe
    210                 215                 220

Leu Arg Arg Leu Asp Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu
225                 230                 235                 240

Lys Thr Trp Tyr Asp His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu
                245                 250                 255

Glu Gln Cys Met Lys Val Leu Val Lys
            260                 265
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<210> 26
<211> 95
<212> PRT
<213> Chlamydia pneumoniae

<400> 26

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Met Leu Ala Phe Phe Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr
  1               5                  10                  15

Ser Tyr Gln Ser Leu Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile
            20                  25                  30

Ile Leu Ala Ser Ile Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala
        35                  40                  45

Thr Gln Ile Gln Glu Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val
    50                  55                  60

Ile Phe Gly Thr Leu Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile
65                  70                  75                  80

Leu Arg Phe Ala Gly Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys
                85                  90                  95
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